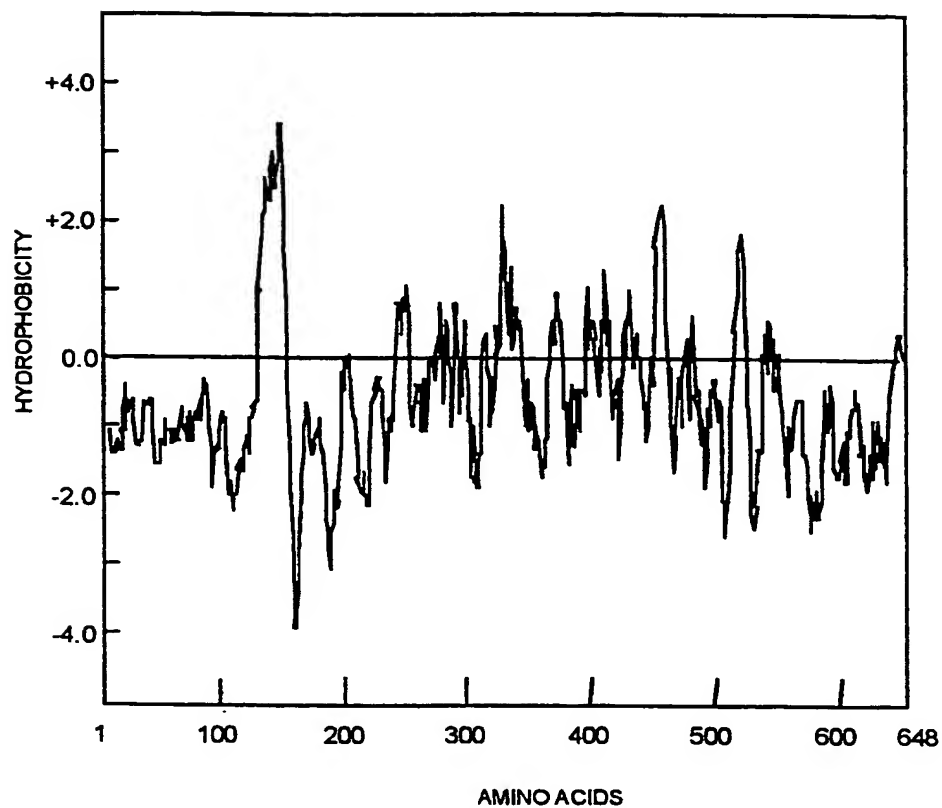


A.

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 A P P P T T P S S P P P P P S T I P T S P
 145 CCTCCTTCTTCTCGCTCTACACCTTCTGCTCTCTCTCCATCTCCACCAACTCCATCTACG 204
 P P S S R S T P S A P P P S P P T P S T
 205 CCGGATCTCCACCTCTCTTCTCTCAGCGCTCTCCACCCGCTCCAACCTACGCCCGGATCT 264
 P G S P P P L P Q P S P P A P T T P G S
 265 CCACCCGACCTGTTACTCTCTCTACTCGAAACCTCCACCTTCAGTCCCAAGGACCACTG 324
 P P A P V T P P T R N P P P S V P G P P
 325 TCCAATCTTTCACGCGAAGGAGGATCTCTCTGACCTCCATCTTCTCTCTCGCCGCCGTCT 384
 S N P S R E G G S P R P P S S P S P P S
 385 CTTCTTCCGAGGTTTATCAACAGGAGTGGTGGTGGGAATCGCCATCGGAGGAGTCTCT 444
 P S S D G L S T G V V V G I A I O G V A
 445 CTGCTTGTGATAGTACTCTGATTTGCTCTCTCTGTAAGAAAGAAACGACGAGAGAGAGAAA 504
 L L V I V T L I C L L C K K K R R R D E
 505 GAAGATGCTTACTATGTTCTCTCGCCACCTCTCTCTGTTCCAAAAGCCGAGGAGGACCTTAC 564
 E D A Y Y V P P P P P P P Q P K A G G P Y
 565 GGTGGACAGCAGCAACAATGCGGCAACAAACGCAACACCACTCAGATCATGTCGTG 624
 G G Q Q Q Q W R Q Q N A T P P S D H V V
 625 ACCTCACTACCAACCACTTAAGGCTCCATCTCCACCAAGGCAACCTCTCTCACTCTCA 684
 T S L P P P P K A P S P P R Q P P P P
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 P P S P G L V L G F S K S T F T Y E E L
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 A R A T N 'Q E S E A N L L L O O O O F O Y
 865 GTGCACAAAGGTGTTGCTTGTGCTAGTGGGAAAGAGTTGCTGTGAAAGGATTGAAAGTTGGG 924
 V H K O V L P S 'O K E V A V F O L K V O
 925 AGTGGTCAGGAGAGAGAGGAGTTTCAGGAGAGGTTGAGATCATCAGCAGAGTTCAACAC 984
 S O 'O G E R E F O A E V E I I S R V 'H H
 985 AGGCATCTGTTCTCTTGTGTTATGTCATCGCGGTGCCAAAGGATTGCTTGTCTAT 1044
 R H L V S L V G Y C I A 'Q A K R L L V Y
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 1105 GAATGGAGCACCAGATTGAAAGATTGCTCTTGGATCTGCTAAAGGACTTCTTATCTTCA 1164
 E W S T R L K I A L O S A R O L S Y L H
 1165 GAAGATTGCAATCTAAATCATTACCGTGATATCAAGGCTTCAACATATTGATAGAT 1224
 E D C N P K J I H R D I R A S N I L I D
 1225 TTCAAGTTTGAAGCTAAGGTTGCTGATTTGCTTGTCTTGAAGATTGCTTGTATACAAAC 1284
 F K E 'E A E V A D F O L A K I A S T N
 1285 ACOCATGTATCAACACGTGTGATGGGAACCTTGGGTACTTGGCTCCGGAATACGCTGCA 1344
 T H V 'S T R V M Q T F O Y L A P E X 'A A
 1345 AGCGGAAAGCTCACGGAGAAAGTCTGACGTTTCTCATTTGGCGTTGTGCTTTTGGAGCTC 1404
 S O K L T E K S D V F S F G V V L L E L
 1405 ATTACTGGACGTCGACCGTTGATGCTCAACAATGCTATGTAGATGACAGCTTAGTTGAC 1464
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 E O N' V S L S D L N E G M R P O G S N V
 1705 TACAGCTCATACGGAGGAGACCGATTATGACTCGAGCCAGTACAATGAAGACATGAAG 1764
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 1765 AAGTTTAGGAAATGGCACTTGGAACTCAAGAGTACAACGCCACGGGTGAGTACAGTAAT 1824
 K F R K M A L G T Q E Y N' A T G E Y S N
 1825 CCGACCAAGTACTATGGACTGTACCCTGCTGTTCAAGCAGCGAGGCGCAACCAACACGC 1884
 P T S D Y G L Y P S G S S S E G Q T T R
 1885 GAAATGGAGATGGGAAAGATTAAAGAGAACCGGTCAAGGTTATAGTGGACCTTCTCTTAA 1944
 E M E M G K I K R T G Q O Y S G P S L .

Figure 1A

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B.**Figure1B****2/26**



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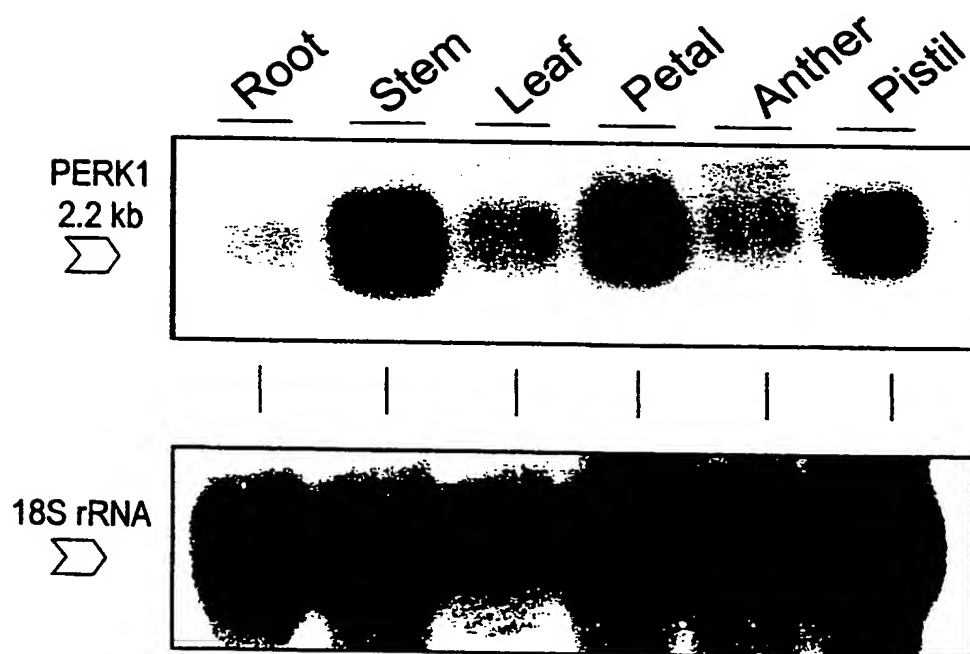
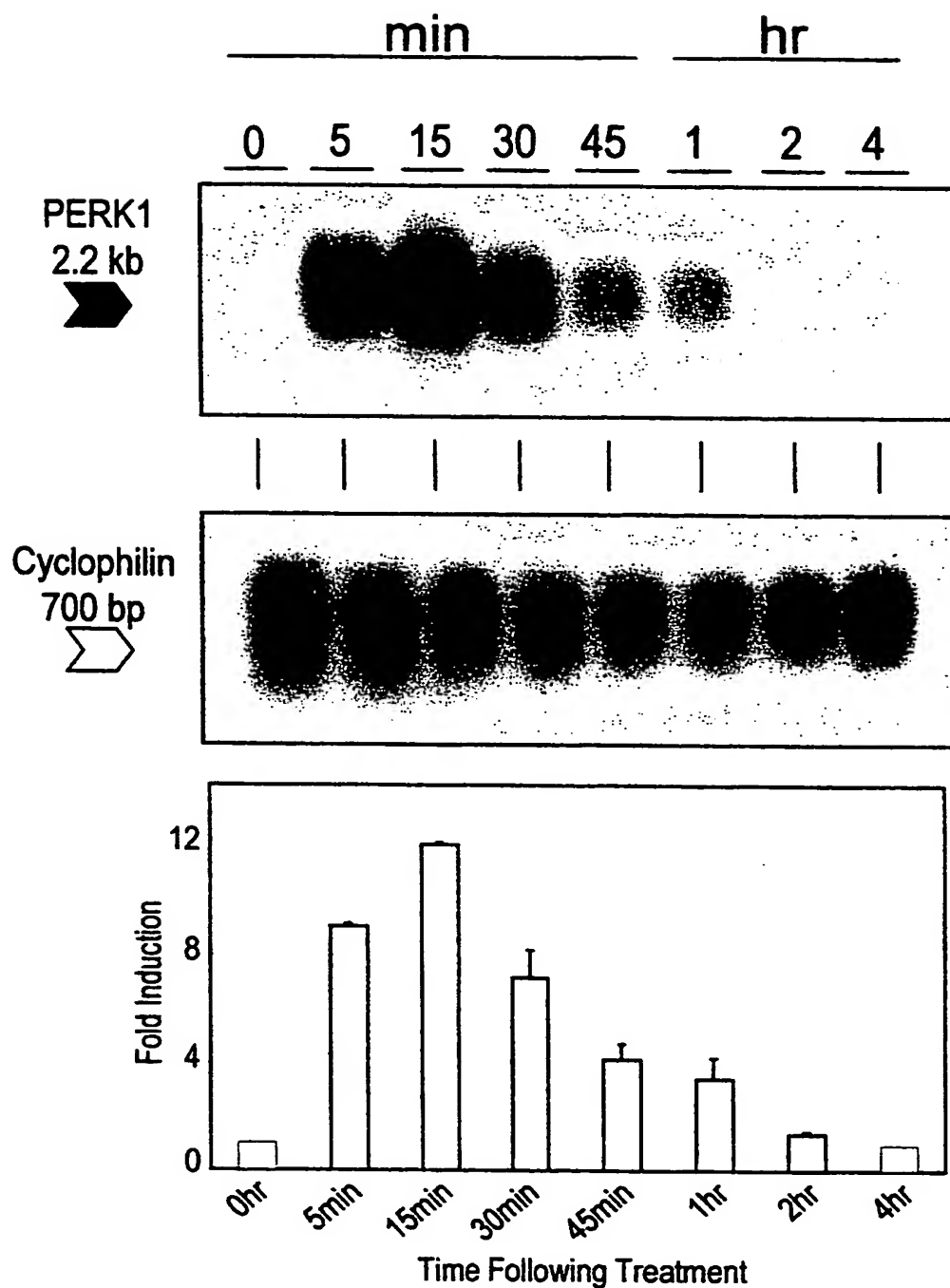


Figure 3
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A.**Figure 4A**

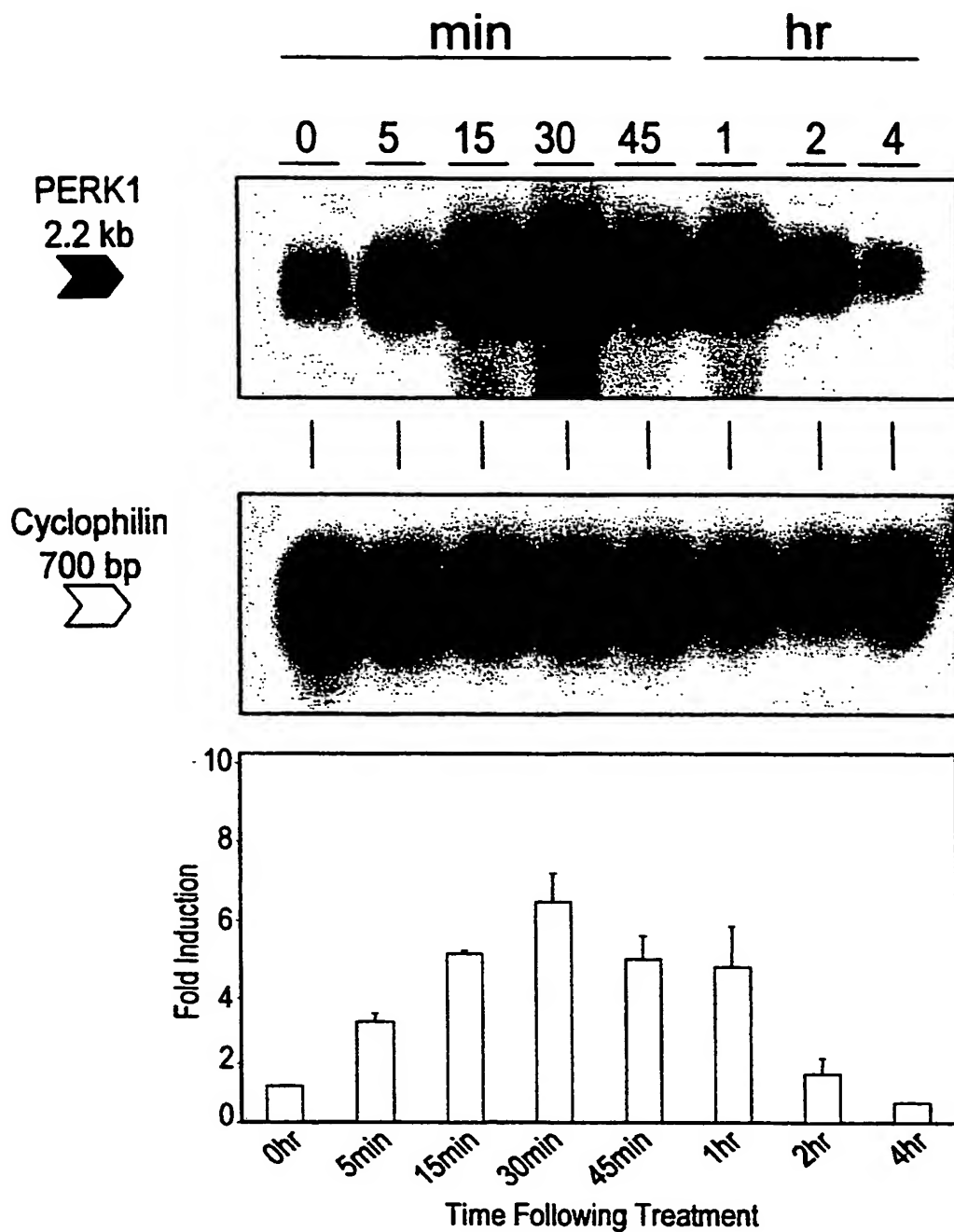
B.

Figure 4B

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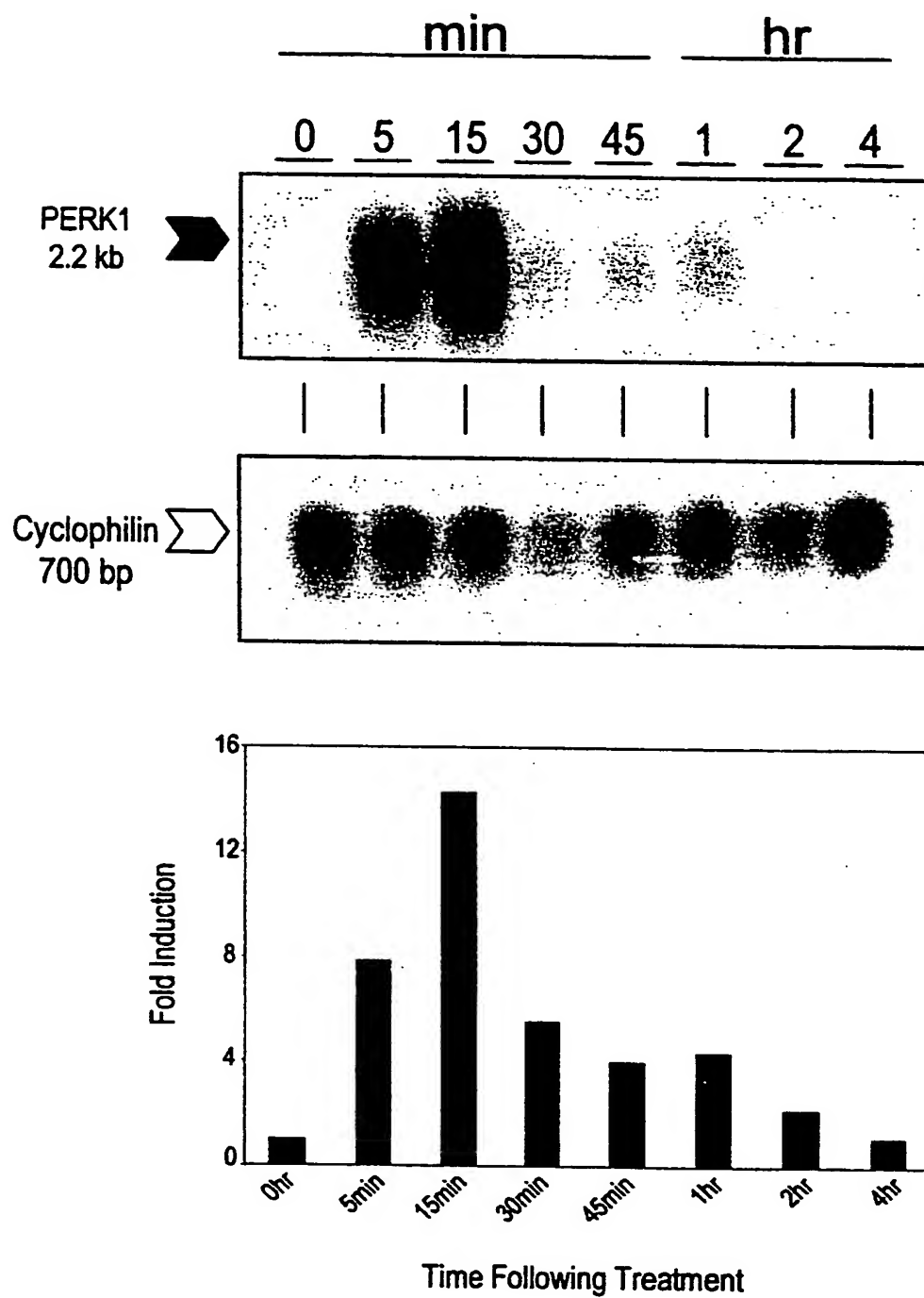


Figure 4a
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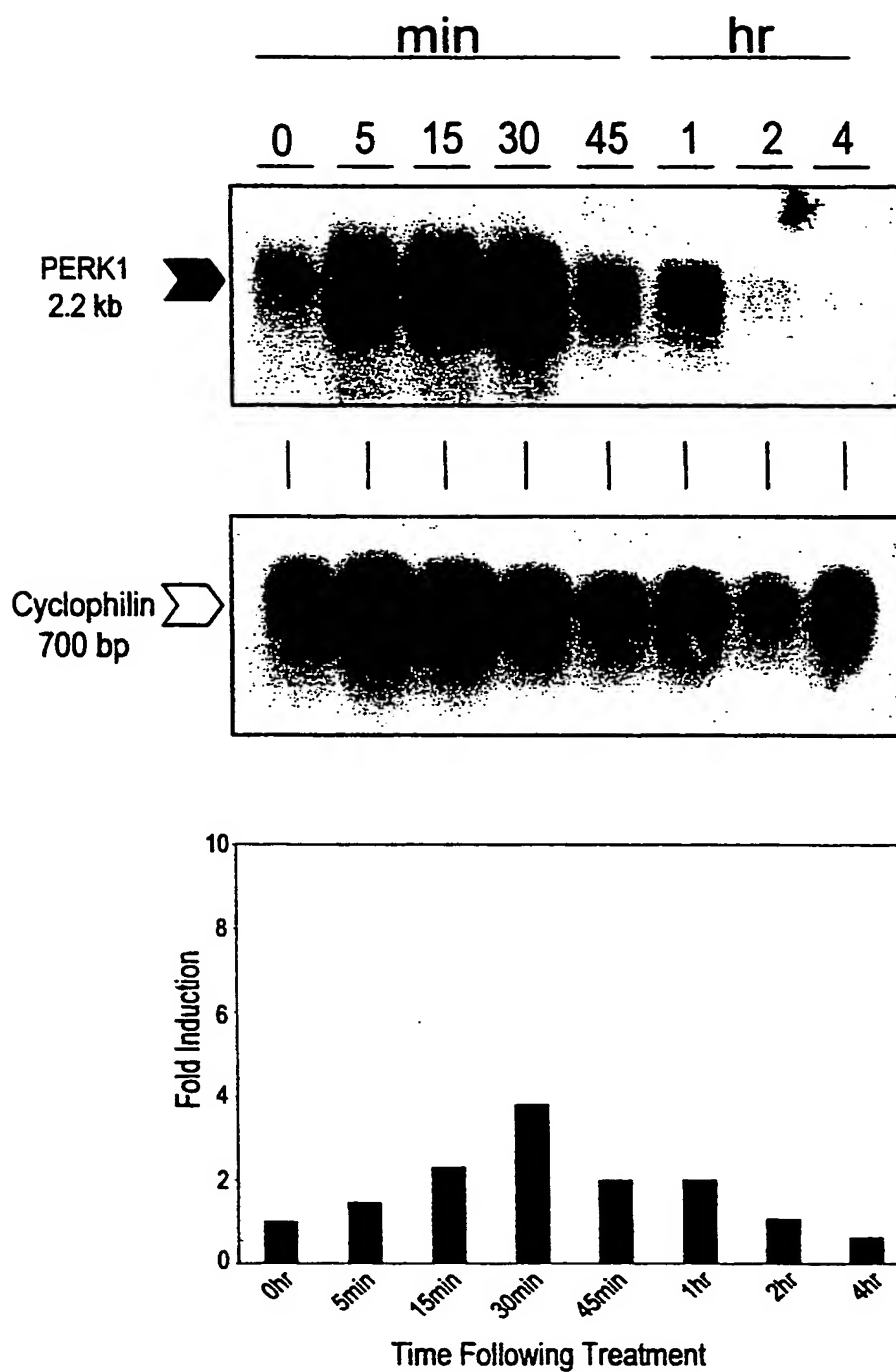
A.

Figure 4b(A)

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SUBSTITUTE SHEET (RULE 26)

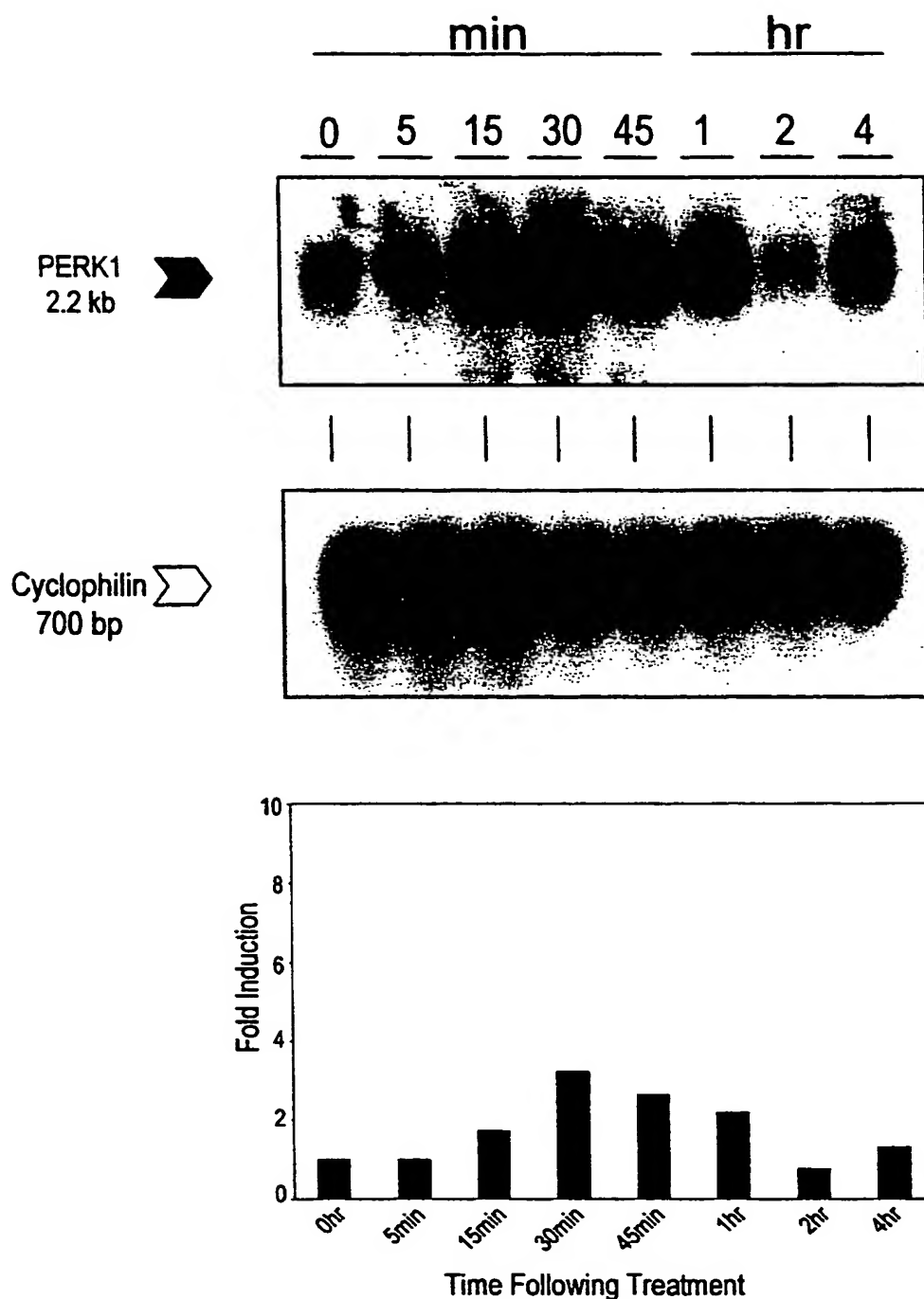
B.

Figure 4b(B)

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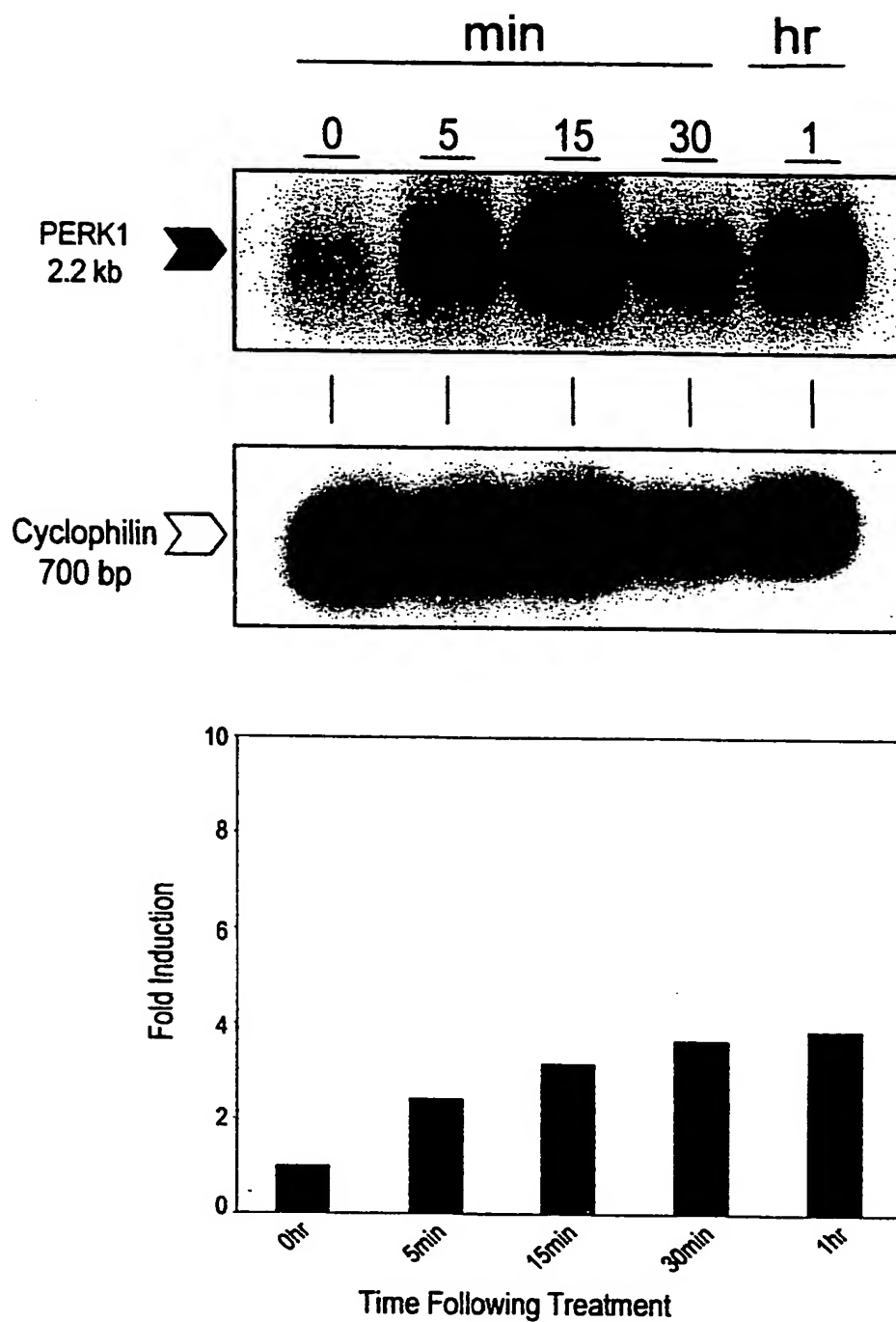


Figure 4c

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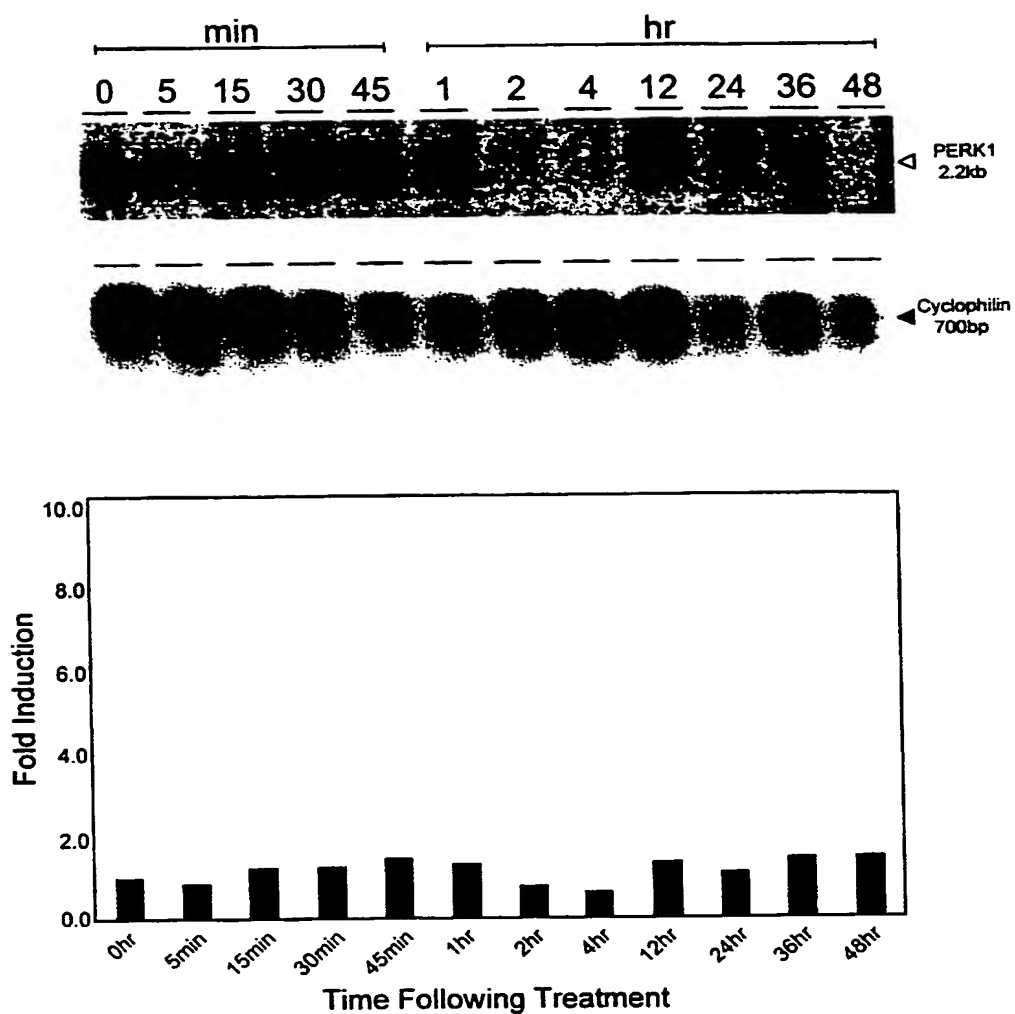
A.

Figure 5A
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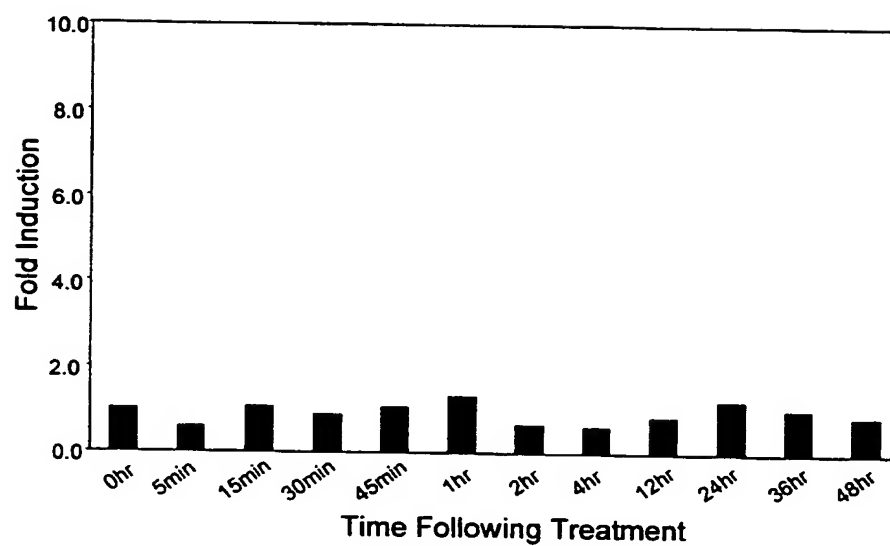
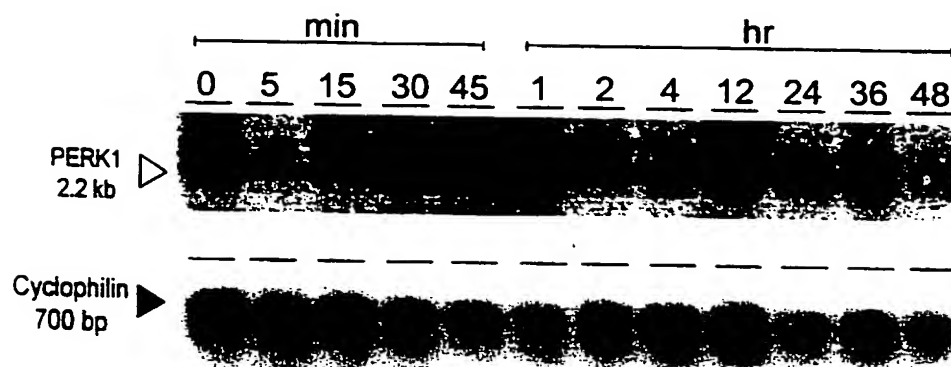
B.

Figure 5B
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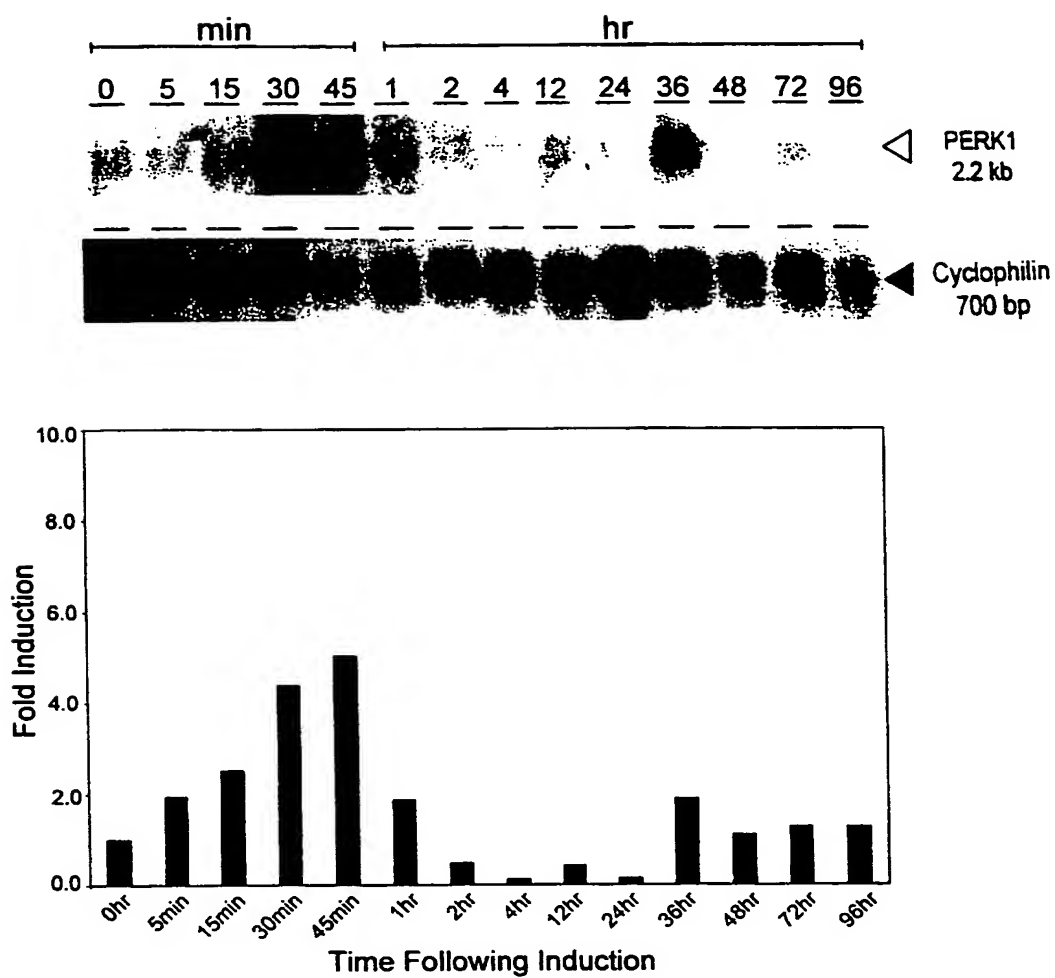
A.

Figure 6A
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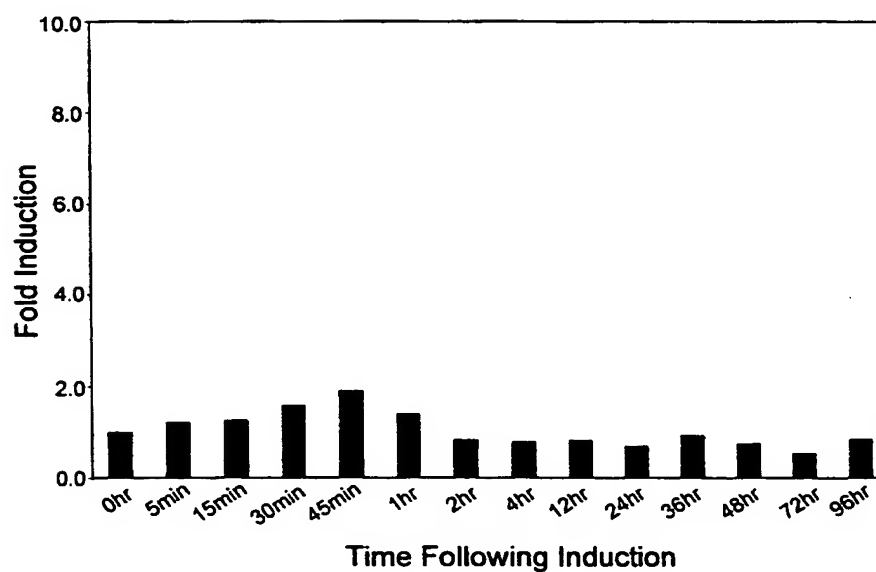
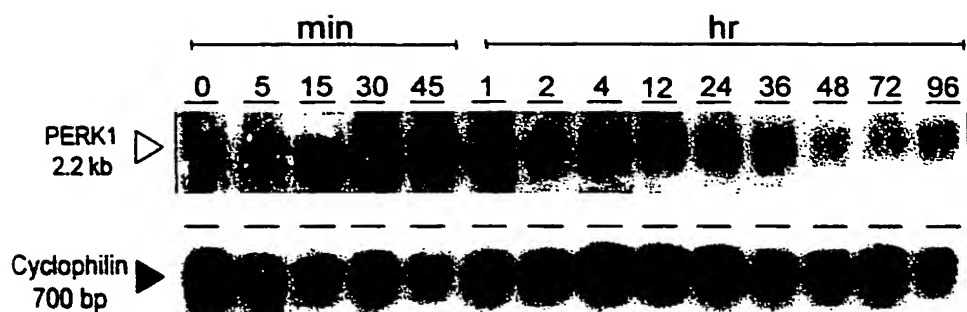
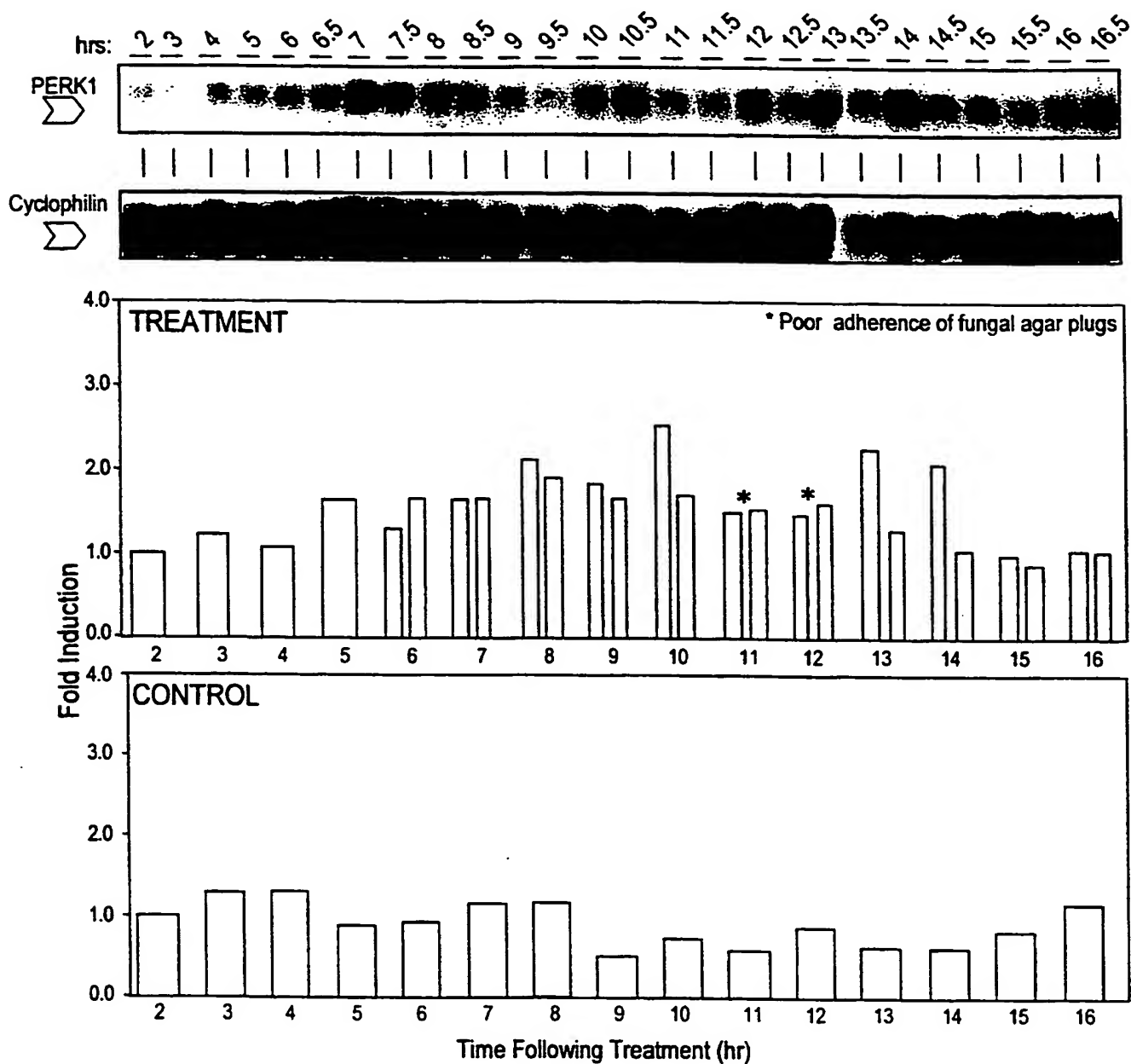
B.

Figure 6B
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Fungal pathogen : *Sclerotinia sclerotiorum*Figure 7
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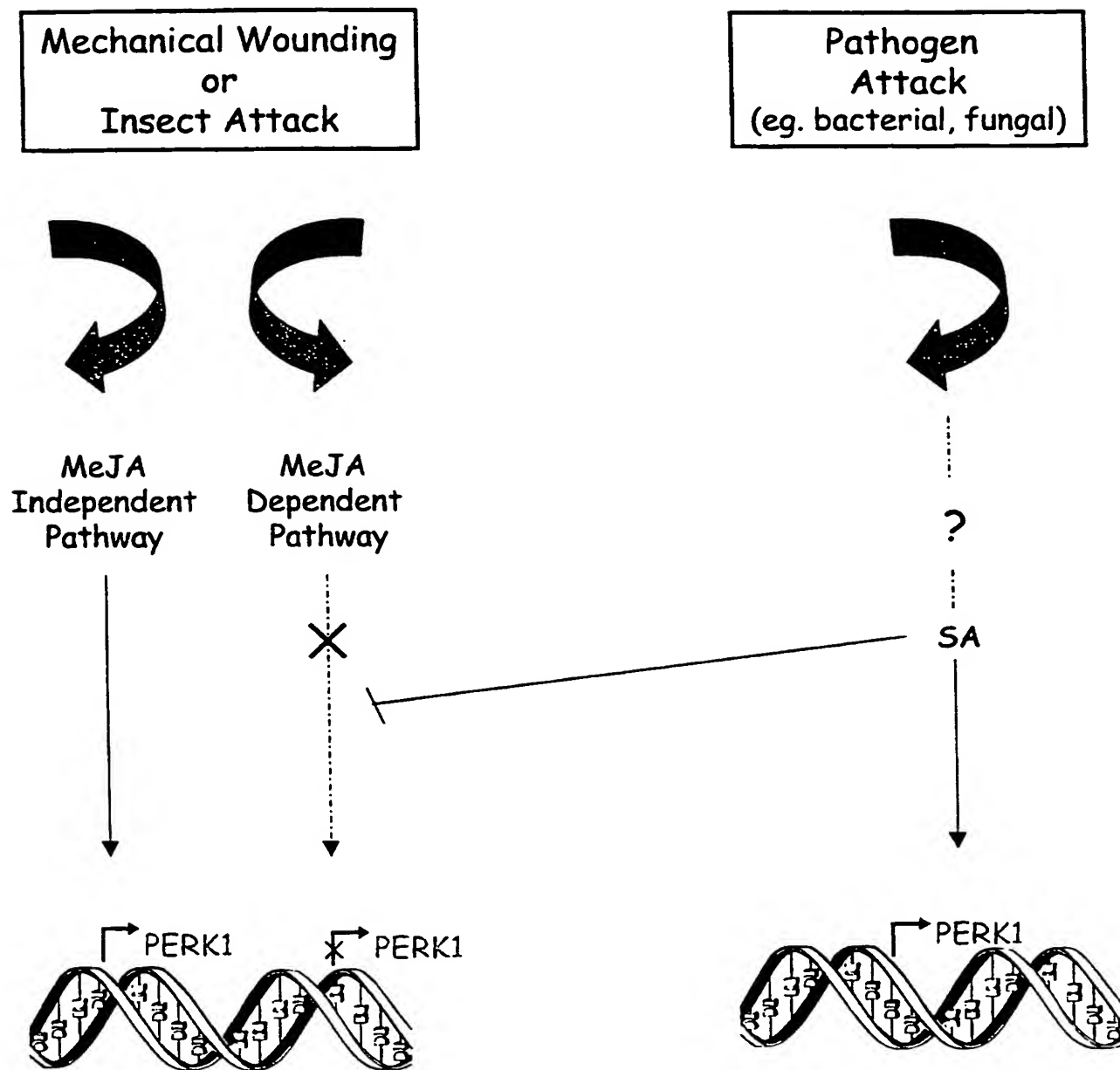
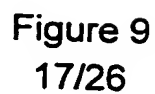
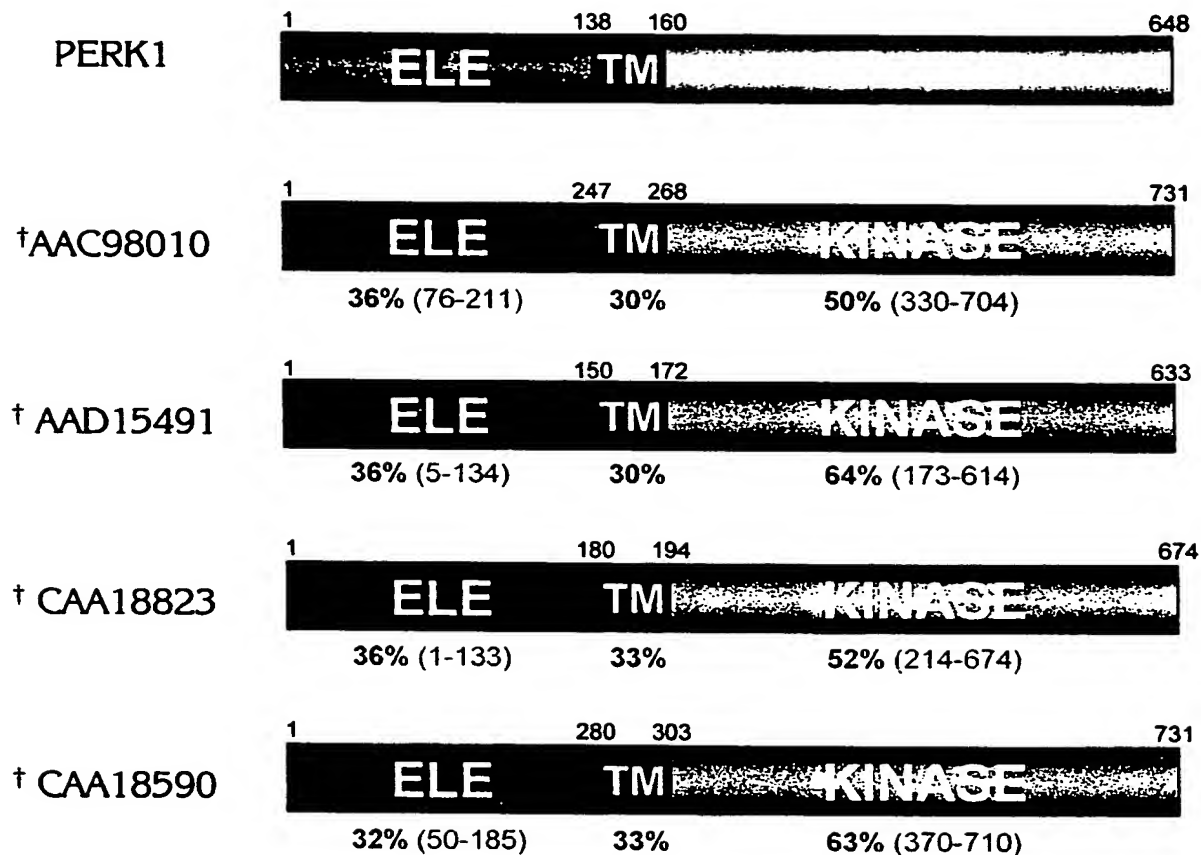


Figure 8
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All have no signal peptide and predicted to be Type1b integral membrane proteins

† Predicted proteins from the Arabidopsis genome sequencing project.

ELE: Extensin-like extracellular ; TM: Transmembrane domain ; Red = sequence identity to PERK1 domain

	PERK1	ACC98010	AAD15491	CAA18823	CAA18590	
PERK1		50%	64%	52%	63%	
ACC98010	36%		54%	50%	52%	Kinase Domains
AAD15491	36%	25%		63%	51%	
CAA18823	36%	29%	27%		60%	
CAA18590	32%	36%	30%	27%		
						ELE Domains

Figure 10
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TAGAAAAAA AAAATGTCAG ACTTAGGCCG GTCGCCGAGT TCTTCACCAC CAGCACCACC
AGCTGATACC GTCCTCCAC CAGAGACTCC ATCAGAAAAC TCAGCTCTTC CACCTGTTGA
TTCTCTCTCT CAGTGTCCAC CAGCTGATTC ATCATCAACA CCGCCGCTGT CAGAACCATC
CACTCTCTCT CCAGATTCCAG AGCTTCCTCC TTTACCTTCG ATTCTCTCTC CGCTAACAGA
TTCTCCACCT CCACCTTCCG ATTCTTCTCC ACCCGTTGAT TCAACCCCTT CTCCGCCGCC
ACCGACGTCA AACGAATCTC CTCTCTCTCC AGAAGATTCC GAAACACCAC CTGCTCCACC
AAATGAATCC AATGACAACA ACCCTCTCTCC GTCTCAAGAT CTTCAATCGC CTCTCCATC
GTCGCCGTCG CCGAATGTAG GACCCACAAA CCCGGAATCA CCACCGTTAC AATCTCTCTC
AGCTCCACCA GCATCAGATC CTACAAATTC ACCGCCAGCT TCACCATTAG ACCCTACCAA
TCCTCCCCCA ATACAACCAT CAGGACCAGC CACTTCTCTT CCGGCTAATC CCAACGCTCC
GCCGAGCCCA TTCCCCACAG TACCACCAA AACTCCTTCT AGTGGACCTG TGGTGTCTCC
ATCTCTCACA TCCCCTAGTA AAGGAACTCC TACTCCAAAC CAAGGCAATG GAGATGGCGG
TGGCGGTGGT GCGCGCTATC AAGGGAAGAC TATGGTTGGT ATGGCTGTAG CCGGTTTCGG
AATCATGGCG CTTATAGGCG TTGTGTCTT AGTGAGAAGA AAGAAAAAGA GAAACATTGA
TAGCTATAAT CACTCACAGT ACTTGCCACA TCCCAATTC TCTGTAAAT CAGGTTTAA
AATCTCACCT TTATCTCTCT CTGATCATCT TCTATGTGCT TGAATCATCT CTCTGACTAT
CTTTGCTTTT GATGTAGATG GATTCTTATA CGGTCAAGAT CCAGGTAAAG GATACTCTCT
TGGTCTAAT GGTTCATGT ATAACAATC ACAGCAACA CAATCCTCTA TGGGAAACAG
TTATGGTACA GCTGGTGGTG GTTATCTCA TCATCAAATG CAATCAAGTG GCACACCTGA
CTCTGCTATA CTCGGAAGTG GCCAGACTCA TTTCAGTTAC GAAGAGCTTG CTGAGATAAC
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TGACCGTGAA TTCAAAGCAG AGGTTGAGAT CATCAGCCGC GTTCATCATC GCCATTGGT
CTCTCTGGTT GGTACTGCA TTTCAGACCA GCATAGATTG CTTATCTATG AGTATGTTTC
TAATCAAACC TTGGAGCATC ATTGTCATGG TGAGTGACTT GTTACCATT TCGTTATAGA
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TGCCAGTTTT AGAGTGGTCT AAGAGAGTCC GGATCGCTAT AGGATCAGCC AAAGGGTTGG
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ATGCACTTCA TAGTTTAAAC AGAAGCCAAA AATCATATCC TGTTTTATT TTACAGGTCA
TCCGAAAATC ATTCACAGAG ATATAAAGTC AGCAAATATT CTCTAGATG ATGAATATGA
AGCTCAGGCA ATAATGAAAT CCTCCTTTTC GTTAAATCTA TCTATGACT GTAAAGTTTT
AGTTAATGAG ACTTGTCTG TTTTTGGAT GTTTAGGTTG CTGATTTTGG ACTTGCTAGA
CTCAATGATA CAACACAAAC TCATGTTTCA ACTCGGGTTA TGGGAACCTT CCGGTAAGCA
AACATTATC ACAAACTCTA CTCCAAACT GGACCTTATT GATCCAATGC CTGATGAAAA
GTTTGTATA TATGGCTTGA GGCAACAAAT TGGATCAAAC CTGAATCTTT ATTGATCGTA
TGGCTGCATG ACATGTTTGG TGTTAAGGTA CCTAGCGCCG GAATATGCAT CAAGTGGAAA
ATTGACTGAT AGATCCGATG TATTCTCATT CGGGGTGTGTT CTCTAGAGC TTGTAACCTG
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CATCTGAAAA CTTATCTACT CTTGAAATA AGGTTGTGAG AGCAATTGGAC TGCGACGGAG
ACTCGGGAGA TATTAGCAAC GGAATCAAAA TTGGGCAAAG CACAATTAT GACTCAGGGC
AATACAATGA AGACATTATG AAATTCAGGA AAATGGCGTT TGGTGGTGAT AACAGCGTAG
AGTCAGGATT GTACAGTGA AACTACTCTG CAAAAGCTC TTCAGATTTC TCAGGGAATG
AATCTGAGAC TCGGCCTTTC AACACCGAC GGTTCTGATC ATACAATAGG TGAAAGTAAC

Figure 11A

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SUBSTITUTE SHEET (RULE 26)

1	M	S	D	L	G	E	S	P	S	S	S	P	P	A	P	P	A	D	T	A	20
1	ATG	TCA	GAC	TTA	GGC	GAG	TCG	CCG	AGT	TCT	TCA	CCA	CCA	GCA	CCA	CCA	GCT	GAT	ACC	GCT	60
21	P	P	P	E	T	P	S	E	N	S	A	L	P	P	V	D	S	S	P	P	40
61	CCT	CCA	CCA	GAG	ACT	CCA	TCA	GAA	AAC	TCA	GCT	CTT	CCA	CCT	GTT	GAT	TCC	TCT	CCT	CCT	120
41	S	P	P	A	D	S	S	S	T	P	P	L	S	E	P	S	T	P	P	P	60
121	AGT	CCA	CCA	GCT	GAT	TCA	TCA	TCA	ACA	CCG	CCG	CTG	TCA	GAA	CCA	TCC	ACT	CCT	CCT	CCA	180
61	D	S	Q	L	P	P	P	L	P	S	I	L	P	P	L	T	D	S	P	P	80
181	GAT	TCA	CAG	CTT	CCT	CTT	TCA	CCT	TCG	ATT	CTT	CCT	CCG	CTA	ACA	GAT	TCT	CCA	CCT	CCA	240
81	P	S	D	S	S	P	P	V	D	S	T	P	S	P	P	P	P	T	S	N	100
241	CCT	TCC	GAT	TCT	TCT	CCA	CCC	GTT	GAT	TCA	ACC	CCT	TCT	CCG	CCA	CCG	CCA	CCG	ACG	TCA	300
101	E	S	P	S	P	P	E	D	S	E	T	P	P	A	P	P	N	E	S	N	120
301	GAA	TCT	CCT	TCT	CCT	CCA	GAA	GAT	TCC	GAA	ACA	CCA	CCT	GCT	CCA	CCA	AAT	GAA	TCC	AAT	160
121	D	N	N	P	P	P	S	Q	D	L	Q	S	P	P	P	S	S	P	S	P	140
361	GAC	AAC	AAC	CCT	CCT	CCG	TCT	CAA	GAT	CTT	CAA	TCG	CCT	CCT	CCA	TCG	TCG	CCG	TCG	CCG	420
141	N	V	G	P	T	N	P	E	S	P	P	L	Q	S	P	P	A	P	P	A	160
421	AAT	GTA	GGA	CCC	ACA	AAC	CCG	GAA	TCA	CCA	CCG	TTA	CAA	TCT	CCT	CCA	GCT	CCA	GCA	GCA	480
161	S	D	P	T	N	S	P	P	A	S	P	L	D	P	T	N	P	P	P	I	180
481	TCA	GAT	CCT	ACA	AAT	TCA	CCG	CCA	GCT	TCA	CCA	TTA	GAC	CCT	ACC	AAT	CCT	CCC	CCA	ATA	240
181	Q	P	S	G	P	A	T	S	P	P	A	N	P	N	A	P	P	S	P	F	200
541	CAA	CCA	TCA	GGA	CCA	GCC	ACT	TCT	CCT	CCG	GCT	AAT	CCC	AAC	GCT	CCG	CCG	AGC	CCA	TTC	260
201	P	T	V	P	P	K	T	P	S	S	G	P	V	V	S	P	S	L	T	S	280
601	CCC	ACA	GTA	CCA	CCC	AAA	ACT	CCT	TCT	AGT	GGA	CCT	GTG	GTG	TCT	CCA	TCT	CTC	ACA	TCC	340
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661	CCT	AGT	AAA	GGA	ACT	CCT	ACT	CCA	AAC	CAA	GGC	AAT	GGA	GAT	GGC	GGT	GGC	GGT	GGT	GGC	460
241	G	Y	Q	G	K	T	M	V	G	M	A	V	A	G	F	A	I	M	A	L	520
721	GGC	TAT	CAA	GGG	AAG	ACT	ATG	GTT	GGT	ATG	GCT	GTA	GCC	GGT	TTC	GCA	ATC	ATG	CGC	CTT	580
261	I	G	V	V	F	L	V	R	R	K	K	K	R	N	I	D	S	Y	N	H	640
781	ATA	GGC	GTT	GTG	TTT	TTA	GTG	AGA	AGA	AAG	AAA	AAG	AGA	AAC	ATT	GAT	AGC	TAT	AAT	CAC	700
281	S	Q	Y	L	P	H	P	N	F	S	V	K	S	D	G	F	L	Y	G	Q	760
841	TCA	CAG	TAC	TTG	CCA	CAT	CCC	AAT	TTC	TCT	GTT	AAA	TCA	GAT	GGA	TTC	TTA	TAC	GGT	CAA	820
301	D	P	G	K	G	Y	S	S	G	P	N	G	S	M	Y	N	N	S	Q	Q	880
901	GAT	CCA	GGT	AAA	GGA	TAC	TCC	TCT	GGT	CCT	AAT	GGT	TCA	ATG	TAT	AAC	AAT	TCA	CAG	CAA	940
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961	CAA	CAA	TCC	TCT	ATG	GGA	AAC	AGT	TAT	GGT	ACA	GCT	GGT	GGT	GGT	TAT	CCT	CAT	CAT	CAA	1060
341	M	Q	S	S	G	T	P	D	S	A	I	L	G	S	G	Q	T	H	F	S	1120
1021	ATG	CAA	TCA	AGT	GGC	ACA	CCT	GAC	TCT	GCT	ATA	CTC	GGA	AGT	GGC	CAG	ACT	CAT	TTC	AGT	1180
361	Y	E	E	L	A	E	I	T	Q	G	P	A	R	K	N	I	L	G	E	G	1240
1081	TAC	GAA	GAG	CTT	GCT	GAG	ATA	ACA	CAA	GGC	TTT	GCT	CGC	AAA	AAC	ATT	CTT	CGA	GAA	GGC	1300
381	G	F	G	C	V	Y	K	G	T	L	Q	D	G	K	V	V	A	V	K	Q	1360
1141	GGA	TTT	GGA	TGT	GTC	TAT	AAA	GGT	ACA	TTG	CAG	GAT	GGT	AAA	GTT	GTT	CGC	GTT	AAG	CAG	1420
401	L	K	A	G	S	G	Q	G	D	R	E	F	K	A	E	V	E	I	I	S	1480
1201	CTT	AAA	GCT	GGA	AGT	GGA	CAA	GGT	GAC	CGT	GAA	TTC	AAA	GCA	GAG	GTT	GAG	ATC	ATC	AGC	1540
421	R	V	H	H	R	H	L	V	S	L	V	G	Y	C	I	S	D	Q	H	R	1600
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441	L	L	I	Y	E	Y	V	S	N	Q	T	L	E	H	H	L	H	E	W	S	1720
1321	TTG	CTT	ATC	TAT	GAG	TAT	GTT	TCT	AAT	CAA	ACC	TTG	GAG	CAT	CAT	TTG	CAT	GAG	TGG	TCT	1780
461	K	R	V	R	I	A	I	G	S	A	K	G	L	A	Y	L	H	E	D	C	1840
1381	AAG	AGA	GTC	CGG	ATC	GCT	ATA	GGA	TCA	GCC	AAA	GGG	TTG	GCA	TAT	CTT	CAC	GAA	GAC	TGT	1900
481	H	P	K	I	I	H	R	D	I	K	S	A	N	I	L	L	D	D	E	Y	1960
1441	CAT	CCG	AAA	ATC	ATT	CAC	AGA	GAT	ATA	AAG	TCA	GCA	AAT	ATT	CTT	CTA	GAT	GAT	GAA	TAT	2020
501	E	A	Q	A	I	M	K	S	S	F	S	L	N	L	S	Y	D	C	K	V	2080
1501	GAA	GCT	CAG	GCA	ATA	ATG	AAA	TCC	TCC	TTT	TCG	TTA	AAT	CTA	TCT	TAT	GAC	TGT	AAA	GTT	2140
521	L	V	A	D	F	G	L	A	R	L	N	D	T	T	Q	T	H	V	S	T	2200
1561	TTA	GTT	GCT	GAT	TTT	GGA	CTT	GCT	AGA	CTC	AAT	GAT	ACA	ACA	CAA	ACT	CAT	GTT	TCA	ACT	2260
541	R	V	M	G	T	F	G	Y	L	A	P	E	Y	A	S	S	G	K	L	T	2320
1621	CGG	GTT	ATG	GGA	ACC	TTC	GGG	TAC	CTA	GCG	CCG	GAA	TAT	GCA	TCA	AGT	GGA	AAA	TTG	ACT	2380
561	D	R	S	D	V	P	S	F	G	V	V	L	L	E	L	V	T	G	R	K	2440
1681	GAT	AGA	TCC	GAT	GTA	TTC	TCA	TTC	GGG	GTT	GTT	CTC	TTA	GAG	CTT	GTA	ACT	GGA	CGG	AAA	2500
581	P	V	D	Q	T	Q	P	L	G	E	E	S	L	V	E	W	A	R	P	L	2560
1741	CCA	GTT	GAC	CAG	ACT	CAG	CCT	CTA	GGA	GAA	GAG	AGT	TTG	GTT	GAA	TGG	CGC	CGC	CCG	CTG	2620
601	L	L	K	A	I	E	T	G	D	L	S	E	L	I	D	T	R	L	E	K	2680
1801	CTT	CTC	AAA	GCC	ATT	GAG	ACC	GGA	GAT	TTA	AGC	GAA	CTG	ATT	GAT	ACA	CGG	CTT	GAA	AAG	2740
621	R	Y	V	E	H	E	V	P	R	M	I	E	T	A	A	A	C	V	R	H	2800
1861	CGT	TAT	GTG	GAG	CAT	GAA	GTC	TTC	AGA	ATG	ATC	GAG	ACA	GCC	GCT	GCA	TGT	GTT	AGA	CAT	2860
641	S	G	P	K	R	P	R	M	V	Q	V	V	R	A	L	D	C	D	G	D	2920
1921	TCT	GGT	CCA	AAA	CGC	CCA	CGC	ATG	GTT	CAG	GTT	GTG	AGA	CTT	GAC	TTC	GAC	TCA	GGG	CAA	2980
661	S	G	D	I	S	N	G	I	K	I	G	Q	S	T	T	Y	D	S	G	Q	3040
1981	TCG	GGA	GAT	ATT	AGC	AAC	GGA	ATC	AAA	ATT	GGG	CAA	AGC	ACA	ACT	TAT	GAC	TCA	GGG	CAA	3100
681	Y	N	E	D	I	M	K	P	R	K	M	A	P	G	G	D	N	S	V	E	3160
2041	TAC	AAT	GAA	GAC	ATT	ATG	AAA	TTC	AGG	AAA	ATG	CGG	TTT	GGT	GGT	GAT	AAC	AGC	GTA	GAG	3220
701	S	G	L	Y	S	G	N	Y	S	A	K	S	S	S	D	F	S	G	N	E	3280
2101	TCA	GGA	TTG	TAC	AGT	GGA	AAC	TAC	TCT	GCC	AAA	AGC	TCT	TCA	GAT	TTC	TCA	GGG	AAT	GAA	3340
721	S	E	T	R	P	F	N	N	R	P	*										3400
2161	TCT	GAG	ACT	CGG	CCT	TTC	AAC	AAC	CGA	CGG	TTC	TGA									3460

Figure 11B

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SUBSTITUTE SHEET (RULE 26)

GAAAAATTTG ATCTCCGATG GCTTCTTCTC CTGAATCTGC TCCTCCAACA AACTCCACCT
 CTTCTCCATC TCCACCGTCT AATACCAATT CAACCACCTC TTCTCCGCCG GCTCCGTCTC
 CTCCTTCTCC TACACCTCT CAAGGAGACT CATCATCATC GCCACCTCCT GATTCCACAT
 CTTCCACCAGC TCCACAAGCT CTAACCCTC CTAATTCCTC TAATAACTCT CTTTCCCCTC
 CGTCACAGGG CGGTGGAGGA GAAAGAGGAA ATGGAGGAAA CAATGGTGGC AATGATACTC
 CACCGTCACG CGGCTCTCCT CTTTCTCTC CTCTAGGAG TAATGGAGAT AATGGTGGTA
 GCAGATCATC GCCACCAGGA GACACTGGAG GCTCTCGCTC AGACAACCCT CTTTCTAGCG
 GAGGAAGCAG TGGAGGAGGT GGAGGTGGAA GAAGTAATAC GAATACAGCG ATCATAGTTG
 GTGTATTAGT CGGAGCTGGA CTTTTGATGA TCGTTCTTAT TATTGTGTGT CTTAGACGCA
 AAAAGAAGAG AAAAGACTCC TTCTACCCTG AACCCATGAA AGGTAAAAAC ATATACACAC
 TCTTATGTTT CAACAAATAA GAAGCTTAGA TTCTTTCATA AAATTCAGG AAACCAATAT
 CAATACTATG GAAACAACAA CAACAACAAT GCTTCACAGA ATTATCCGAA TTGGCACCTA
 AATTCACAAG GCCAAAACCA ACAATCTACT GGTGGTTGGG GAGGCGGTGG ACCATCACCG
 CCTCTCTCTC CGCGGATGCC TACAAGCGGA GAAGATTCTT CCATGTACTC AGGCCATCA
 CGCCCAAGTTT TACCTCTCTC TTCGCCTGCT CTAGCCCTCG GATTCAACAA GAGCACTTTT
 ACTTACCAAG AGCTTGCGG TGCAACAGGA GGGTTTACGG ATGCTAACCT TTTGGGACAG
 GGAGGATTG GGTATGTCCA TAAAGGAGTC TTGCCTAGCG GGAAAGAAGT AGCAGTTAAG
 AGTTTAAAAG CGGGTAGCGG ACAAGGAGAG AGGGAGTTTC AAGCTGAGGT CGATATCAIT
 AGCCGTGTGC ATCATCGGTA TCTTGTTTCT TTGGTTGGAT ATTGCATAGC TGATGGACAG
 AGGATGTTGG TTTATGAGTT TGTTCTTAAC AAACTTTGG AATATCATCT TCATGGTTAG
 ACCACTTAA AACTTTGAGT ACTAAGTTTA TTTTCTCTAA TCTATATATT CAAGAAAGTT
 GTAACCTTAA TTTGTTGTTG TAGGGAAAAA TCTTCCGGTA ATGGAGTTCT CCACTAGGTT
 GCGTATCGCC TTAGGTGCTG CGAAAGGACT CGCTTACCTT CACGAAGACT GTAAGTTTTA
 ACATTCACCA TTCTCATTTT CTTAACCAAG TTGCATAAAA CAGAGAAAGC TCTGTCTCTG
 ACTAGTGTTA TCTTTTGGC TGAGAAAATG GTGCAGGCCA TCCTCGGATC ATTACCCGCG
 ACATCAAGTC TGCAAATATT CTCTTGGACT TCAACTTTGA TGCTATGGTG ATAAACTAGT
 AGCTTGCAAT CATCTACGGT TTTTGTGTTA GACTACATTG ATGACATTTT GCATTTGTTT
 ATTACGGTGG CTGATTTTGG ATTAGCTAAG TTAACATCTG ATAACAACAC TCATGTATCT
 ACTCGTGTGA TGGGAACITT CGGGTAAGCG TTTTACCGTA TGATAAGATT GTTCGTGACA
 CTCAAGAAAC ATAACCTTTG TAGACTAATC TACTTTGCTT CTTTCCACAA ACATGTGTAG
 ATATCTAGCT CCAGAATATG CTTCAAGCGG TAAATTAACC GAGAAATCCG ATGTTTCTC
 TTACGGAGTT ATGTTATTGG AACTTATAAC TGGAAAACGA CCGGTTGATA ATAGCATCAC
 CATGGACGAC ACCTTAGTAG ATTGGGTATT CATGCATGTA ACATATGTAT CGTGTATATA
 TGTTTTTCGC CTTTTTCGCG TACTAATGAT CATGAATACA GGCTCGGCCT CTTATGGCTC
 GCGCGCTAGA AGATGGAAAC TTTAATGAGC TCGCAGATGC GAGGCTTGAA GGCAACTACA
 ACCCGCAAGA AATGGCTCGA ATGGTGACTT GTGCCGCTGC TAGCATTCTG CATTGGGGGC
 GTAAACGTCC AAAGATGAGC CAGGTGAATC AAAATTATAA CTAAAAGTCT ATTTTTGTCA
 GAGAATAACA AACAAATGTT GTGGTTTTCA GATAGTAAGA GCGTTAGAAG GAGAAGTGTC
 CTTAGATGCT TTAACGAAG GTGTGAAGCC AGGACACAGT AACGTTTACG GGTATTGGG
 AGCAAGCTCG GATTATAGTC AGACATCTTA CAATGCAGAC ATGAAGAAAT TCAGACAGAT
 AGCTTTGTCT AGCCAAGAAT TCCCAGTCAG TGACTGTGAA GGAACATCTA GTAATGATTC
 TAGAGATATG GGAACATAA GCCCTACTCC TCCAAAATGA GATCGAATCA ATGATTCTGT

Figure 12A
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	M	A	S	S	P	E	S	A	P	P	T	N	S	T	S	S	P	S	P	P	20
1	ATG	GCT	TCT	TCT	CCT	GAA	TCT	GCT	CCT	CCA	ACA	AAC	TCC	ACC	TCT	TCT	CCA	TCT	CCA	CCG	60
21	S	N	T	N	S	T	T	S	S	P	P	A	P	S	P	P	S	P	T	P	40
61	TCT	AAT	ACC	AAT	TCA	ACC	ACC	TCT	TCT	CCG	CCG	GCT	CCG	TCT	CCT	CCT	TCT	CCT	ACA	CCT	120
41	P	Q	G	D	S	S	S	S	P	P	P	D	S	T	S	P	P	A	P	Q	60
121	CCT	CAA	GGA	GAC	TCA	TCA	TCA	TCG	CCA	CCT	CCT	GAT	TCC	ACA	TCT	CCA	CCA	GCT	CCA	CAA	180
61	A	P	N	P	P	N	S	S	N	N	S	P	S	P	P	S	Q	G	G	G	80
181	GCT	CCT	AAC	CCT	CCT	AAT	TCC	TCT	AAT	AAC	TCT	CCT	TCC	CCT	CCG	TCA	CAG	GGC	GGT	GGA	240
81	G	E	R	G	N	G	G	N	N	G	G	N	D	T	P	P	S	R	G	S	100
241	GGA	GAA	AGA	GGA	AAT	GGA	GGA	AAC	AAT	GGT	GGC	AAT	GAT	ACT	CCA	CCG	TCA	CGC	GGC	TCT	300
101	P	P	S	P	P	S	R	S	N	G	D	N	G	G	S	R	S	S	P	P	120
301	CCT	CCT	TCT	CCT	CCT	TCT	AGG	AGT	AAT	GGA	GAT	AAT	GGT	GGT	AGC	AGA	TCA	TCG	CCA	CCA	360
121	G	D	T	G	G	S	R	S	D	N	P	P	S	S	G	G	S	G	G	G	140
361	GGA	GAC	ACT	GGA	GGC	TCT	CGC	TCA	GAC	AAC	CCT	CCT	TCT	AGC	GGA	GGA	AGC	AGT	GGA	GGA	420
141	G	G	G	G	R	S	N	T	N	T	A	I	I	V	G	V	L	V	G	A	160
421	GGT	GGA	GGT	GGA	AGA	AGT	AAT	ACG	AAT	ACA	GCG	ATC	ATA	GTT	GGT	GTA	TTA	GTC	GGA	GCT	480
161	G	L	L	M	I	V	L	I	I	V	C	L	R	R	K	K	K	R	K	D	180
481	GGA	CTT	TTG	ATG	ATC	GTT	CTT	ATT	ATT	GTG	TGT	CTT	AGA	CGC	AAA	AAG	AAG	AGA	AAA	GAC	540
181	S	F	Y	P	E	P	M	K	G	N	Q	Y	Q	Y	Y	G	N	N	N	N	200
541	TCC	TTC	TAC	CCT	GAA	CCC	ATG	AAA	GGA	AAC	CAA	TAT	CAA	TAC	TAT	GGA	AAC	AAC	AAC	AAC	600
201	N	N	A	S	Q	N	Y	P	N	W	H	L	N	S	Q	G	Q	N	Q	Q	220
601	AAC	AAT	GCT	TCA	CAG	AAT	TAT	CCG	AAT	TGG	CAC	CTA	AAT	TCA	CAA	GGC	CAA	AAC	CAA	CAA	660
221	S	T	G	G	W	G	G	G	G	P	S	P	P	P	P	P	R	M	P	T	240
661	TCT	ACT	GGT	GGT	TGG	GGA	GGC	GGT	GGA	CCA	TCA	CCG	CCT	CCT	CCT	CCG	CGG	ATG	CCT	ACA	720
241	S	G	E	D	S	S	M	Y	S	G	P	S	R	P	V	L	P	P	P	S	260
721	AGC	GGA	GAA	GAT	TCT	TCC	ATG	TAC	TCA	GGC	CCA	TCA	CGC	CCA	GTT	TTA	CCT	CCT	CCT	TCG	780
261	P	A	L	A	L	G	F	N	K	S	T	F	T	Y	Q	E	L	A	A	A	280
781	CCT	GCT	CTA	GCC	CTC	GGA	TTC	AAC	AAG	AGC	ACT	TTT	ACT	TAC	CAA	GAG	CTT	GCG	GCT	GCA	840
281	T	G	G	F	T	D	A	N	L	L	G	Q	G	G	F	G	Y	V	H	K	300
841	ACA	GGA	GGG	TTT	ACG	GAT	GCT	AAC	CTT	TTG	GGA	CAG	GGA	GGA	TTT	GGG	TAT	GTC	CAT	AAA	900
301	G	V	L	P	S	G	K	E	V	A	V	K	S	L	K	A	G	S	G	Q	320
901	GGA	GTC	TTG	CCT	AGC	GGG	AAA	GAA	GTA	GCA	GTT	AAG	AGT	TTA	AAA	GCG	GGT	AGC	GGA	CAA	960
321	G	E	R	E	F	Q	A	E	V	D	I	I	S	R	V	H	H	R	Y	L	340
961	GGA	GAG	AGG	GAG	TTT	CAA	GCT	GAG	GTC	GAT	ATC	ATT	AGC	CGT	GTG	CAT	CAT	CGG	TAT	CTT	1020
341	V	S	L	V	G	Y	C	I	A	D	G	Q	R	M	L	V	Y	E	F	V	360
1021	GTT	TCT	TTG	GTT	GGA	TAT	TGC	ATA	GCT	GAT	GGA	CAG	AGG	ATG	TTG	GTT	TAT	GAG	TTT	GTT	1080
361	P	N	K	T	L	E	Y	H	L	H	G	K	N	L	P	V	M	E	F	S	380
1081	CCT	AAC	AAA	ACT	TTG	GAA	TAT	CAT	CTT	CAT	GGG	AAA	AAT	CTT	CCG	GTA	ATG	GAG	TTC	TCC	1140
381	T	R	L	R	I	A	L	G	A	A	K	G	L	A	Y	L	H	E	D	C	400
1141	ACT	AGG	TTG	CGT	ATC	GCC	TTA	GGT	GCT	GCG	AAA	GGA	CTC	GCT	TAC	CTT	CAC	GAA	GAC	TGC	1200
401	H	P	R	I	I	H	R	D	I	K	S	A	N	I	L	L	D	F	N	F	420
1201	CAT	CCT	CCG	ATC	ATT	CAC	CGC	GAC	ATC	AAG	TCT	GCA	AAT	ATT	CTC	TTG	GAC	TTC	AAC	TTT	1260
421	D	A	M	V	A	D	F	G	L	A	K	L	T	S	D	N	N	T	H	V	440
1261	GAT	GCT	ATG	GTG	GCT	GAT	TTT	GGA	TTA	GCT	AAG	TTA	ACA	TCT	GAT	AAC	AAC	ACT	CAT	GTA	1320
441	S	T	R	V	M	G	T	F	G	Y	L	A	P	E	Y	A	S	S	G	K	460
1321	TCT	ACT	CGT	GTG	ATG	GGA	ACT	TTC	GGA	TAT	CTA	GCT	CCA	GAA	TAT	GCT	TCA	AGC	GGT	AAA	1380
461	L	T	E	K	S	D	V	F	S	Y	G	V	M	L	L	E	L	I	T	G	480
1381	TTA	ACC	GAG	AAA	TCC	GAT	GTT	TTC	TCT	TAC	GGA	GTT	ATG	TTA	TTG	GAA	CTT	ATA	ACT	GGA	1440
481	K	R	P	V	D	N	S	I	T	M	D	D	T	L	V	D	W	A	R	P	500
1441	AAA	CGA	CCG	GTT	GAT	AAT	AGC	ATC	ACC	ATG	GAC	GAC	ACC	TTA	GTA	GAT	TGG	GCT	CCG	CCT	1500
501	L	M	A	R	A	L	E	D	G	N	F	N	E	L	A	D	A	R	L	E	520
1501	CTT	ATG	GCT	CGC	GCG	CTA	GAA	GAT	GGA	AAC	TTT	AAT	GAG	CTC	GCA	GAT	GCG	AGG	CTT	GAA	1560
521	G	N	Y	N	P	Q	E	M	A	R	M	V	T	C	A	A	A	S	I	R	540
1561	GGC	AAC	TAC	AAC	CCG	CAA	GAA	ATG	GCT	CGA	ATG	GTG	ACT	TGT	GCC	GCT	GCT	AGC	ATT	CGT	1620
541	H	S	G	R	K	R	P	K	M	S	Q	I	V	R	A	L	E	G	E	V	560
1621	CAT	TCG	GGG	CGT	AAA	CGT	CCA	AAG	ATG	AGC	CAG	ATA	GTA	AGA	GCG	TTA	GAA	GGA	GAA	GTG	1680
561	S	L	D	A	L	N	E	G	V	K	P	G	H	S	N	V	Y	G	S	L	580
1681	TCC	TTA	GAT	GCT	TTA	AAC	GAA	GGT	GTG	AAG	CCA	GGA	CAC	AGT	AAC	GTT	TAC	GGG	TCA	TTG	1740
581	G	A	S	S	D	Y	S	Q	T	S	Y	N	A	D	M	K	K	F	R	Q	600
1741	GGA	GCA	AGC	TCG	GAT	TAT	AGT	CAG	ACA	TCT	TAC	AAT	GCA	GAC	ATG	AAG	AAA	TTC	AGA	CAG	1800
601	I	A	L	S	S	Q	E	F	P	V	S	D	C	E	G	T	S	S	N	D	620
1801	ATA	GCT	TTG	TCG	AGC	CAA	GAA	TTC	CCA	GTC	AGT	GAC	TGT	GAA	GGA	ACA	TCT	AGT	AAT	GAT	1860
621	S	R	D	M	G	T	K	S	P	T	P	P	K	*							634
1861	TCT	AGA	GAT	ATG	GGA	ACT	AAG	AGC	CCT	ACT	CCT	CCA	AAA	TGA							1902

Figure 12B

TCCACCGTTT GAGAAACCCT AATAACAACA TTCAAATGG CGGACTCACC GGTGGATTCA
TCTCCTGCCC CTGAAACCTC AAATGGGACA CCACCGTCAA ACGGAACATC GCCGTCTAAT
GAGTCATCGC CGCCAACACC ACCTTCTTCA CCACCACCAT CATCAATATC TGCTCCTCCG
CCAGATATCT CCGTCTCTTT TTCACCGCCG CCTGCACCAC CAACGCAAGA AACGTCACCT
CCTACATCTC CGTCCTCATC GCCGCCTGTT GTAGCTAATC CGTCACCGCA GACTCCAGAG
AATCCTTCTC CACCTGCACC TGAAGGCTCA ACTCCTGTAA CGCCACCTGC ACCACCACAA
ACACCGTCGA ACCAATCACC GGAAAGACCA ACTCCTCCTT CTCCTGGTGC CAATGATGAC
CGAAACAGAA CCAATGGCGG AAACAACAAC AGAGACGGCT CCACACCATC ACCACCGTCG
TCAGGGAACA GAACTTCCGG TGACGGTGGC TCACCTTCAC CACCTCGGTC GATAAGCCCT
CCTCAGAATA GTGGAGATTG AGACTCATCA TCGGGTAATC ATCCACAAGC CAACATTGGA
TTGATTATTG GAGTCCTTGT AGGAGCAGGG CTTTGCTTC TACTTGCACT GTGTATTTGC
ATCTGTTGCA ACAGGAAGAA GAAGAAGAAA TCTCCTCAGG TCAACCACAT GCACTACTAC
AATAACAATC CTTATGGAGG AGCACCTCA GGTAAATTACA GTTTAGTATA ACTGGAATTT
AATTTGTAGC CTAATGGTGT TTGATTAGGT TTCAGAACGA TCATAGTCTA ATGGTTTCTG
CTAGCTCCAT ATGGCAAAAG GATTAGATTT ATAAGCTAAA GGAGATGTTG CATAGTGTAG
GTAATGGTGG TTATTACAAG GGAACACCTC AAGATCATGT GGTGAATATG GCTGGTCAAG
GAGGTGGGAA TTGGGGTCCA CAGCAACCTG TGTCTGGTCC TCACAGTGAT GCTTCCAATC
TAACCGGTGC AACTGCTATA CCGTCACCTC AAGCTGCAAC TCTTGGTCAC AACCAAAGCA
CTTTCACATA CGATGAAGTG TCCATTGCAA CAGAAGGTTT CGCTCAGTCA AATTTGCTAG
GACAAGGAGG ATTTGGGTAT GTTCATAAAG GAGTTCTGCC TAGTGGCAAA GAAGTTGCAG
TGAAGAGTCT TAAACTTGGA AGTGGACAAG GGAACGCGA GTTTCAGCA GAGGTTGATA
TCATTAGCCG TGTCCATCAT CGTCATCTCG TTTCTCTTGT TGGATATTGC ATCTCTGGTG
GTCAAAGACT TTTGGTTTAT GAGTTTATAC CTAACAACAC TCTTGAATTT CATCTTCATG
GTACATTCACT CTAACAGAAT GTTTTCTTGT ATTAACAAA CTTTAAAGTA TGGTTTCTCT
TTAATCAGGA ACATGATTGA AATTTAGGA AAGGGTCGTC CGGTTTGGGA TTGGCTTACA
AGAGTGAAGA TTGCATTGGG ATCAGCTAGA GGCTTGCAT ATTGCATGA AGACTGTAAG
AAAATCTTTA TCTCACATAT TTGCATCAGT TTCTATCTCG CTCTCTACAA TATTTGAAAG
ATTGTATATG TTACATCAAT TATAGGTCAC CCTCGCATT TCCACAGAGA TATCAAAGCT
GCAAACATTC TTCTTGATTT CAGTTTGGAG ACCAAGGTAT GTGTGTATAT ATCGACTCTT
GTACTACTTT TACTTTCATT GTCTCTCATT TTTGTTTCCA ATCTGTGTCG ATGTGTGTAT
CAGTCTTATT GTGTAAATAT ATGCAGGTGG CAGATTTTGG ATTGGCTAAG CTATCTCAAG
ACAACTATAC TCATGTCTCC ACTCGCGTCA TGGGAACCTT TGGGTAAGCA GCTTTGTAAA
ATGTCTCAAC TCATCCACAC TTATTTAGTT TCTTTCACCT GTTTTAAACA TTTTCTTGGA
TTCAGATACT TAGTCCAGA GTATGCATCA AGCGGAAAGT TATCCGACAA ATCTGATGTT
TTCTCATTG GAGTAATGCT TCTTGAGCTC ATAACCGGAA GACCTCCTCT GGATCTAACT
GGAGAAATGG AAGATAGCTT GGTAGATTGG GTAAGTCGGT CCCCCTCTCT TCGGTTTACT
TGTTTAATCC CAAAACACTT TCCAAAGCAA AAACAGAAAC AAATCTTACT ATTGTTGTTG
CAGGCAAGGC CTTTGTGTTT GAAAGCAGCT CAAGATGGAG ATTACAACCA ATTGGCTGAT
CCACGTCTAG AGCTAAACTA CAGTCATCAA GAGATGGTTC AAATGGCTTC TTGTGCAGCT
GCAGCAATCA GACATTCAGC AAGAAGACGG CCTAAGATGA GCCAGGTTCA AAAACTCATA
CCACTTGTG GTTCTATTGT TATATTTTAA CTCACAATTA ATCTTGATGA TAAATGTGAC
ATACTAATGA ATCTTGAAAC ATGTGTATGG TAAATGAAAA GATTGTACGA GCACTAGAAG
GAGATATGTC AATGGATGAT CTAAGTGAGG GAACAAGACC AGGACAAAGC ACGTACTTGA
GCCCCGGGAG CGTGAGCTCA GAGTATGACG CAAGCTCGTA CACGGCAGAC ATGAAAAAGT
TCAAGAAACT GCGGTTAGAG AATAAAGAAT ATCAAAGCAG TGAATATGGT GGAACAAGTG
AGTATGGCTT AAACCTTCT GCTTCAAGTA GTGAAGAAAT GAATAGAGGC TCAATGAAAC
GCAATCCTCA GCTTTGAAAG AAGAGACAAC ACTTGTGATA ATATTCAGT TTTCTTCTCT

Figure 13A

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1	M	A	D	S	P	V	D	S	S	P	A	P	E	T	S	N	G	T	P	P	20
1	ATG	GCG	GAC	TCA	CCG	GTG	GAT	TCA	TCT	CGT	GCC	CCT	GAA	ACC	TCA	AAT	GGG	ACA	CCA	CCG	60
21	S	N	G	T	S	P	S	N	E	S	S	P	P	T	P	P	S	S	P	P	40
61	TCA	AAC	GSA	ACA	TCG	CCG	TCT	AAT	GAG	TCA	TCG	CCG	CCA	ACA	CCA	CCT	TCT	TCA	CCA	CCA	120
41	P	S	S	I	S	A	P	P	D	I	S	A	S	F	S	P	P	P	A	A	60
121	CCA	TCA	TCA	ATA	TCT	GCT	CCT	CCG	CCA	GAT	ATC	TCC	GCT	TCT	TTT	TCA	CCG	CCG	CCT	GCA	180
61	P	P	T	Q	E	T	S	P	P	T	S	P	S	S	S	P	P	V	V	A	80
181	CCA	CCA	ACG	CAA	GAA	ACG	TCA	CCT	CCT	ACA	TCT	CCG	TCC	TCA	TCG	CCG	CCT	GTT	GTA	GCT	240
81	N	P	S	P	Q	T	P	E	N	P	S	P	P	A	P	E	G	S	T	P	100
241	AAT	CCG	TCA	CCG	CAG	ACT	CCA	GAG	AAT	CCT	TCT	CCA	CCT	GCA	CCT	GAA	GGC	TCA	ACT	CCT	300
101	V	T	P	P	A	P	P	Q	T	P	S	N	Q	S	P	E	R	P	T	P	120
301	GTA	ACG	CCA	CCT	GCA	CCA	CAA	ACA	CCG	TCG	AAC	CAA	TCA	CCG	GAA	AGA	CCA	ACT	CCT		360
121	P	S	P	G	A	N	D	R	N	R	T	N	G	G	N	N	N	R	D		140
361	CCT	TCT	CCT	GGT	GCC	AAT	GAT	GAC	CGA	AAC	AGA	ACC	AAT	GGC	GGA	AAC	AAC	AGA	GAC		420
141	G	S	T	P	S	P	P	S	S	G	N	R	A	T	S	G	D	G	G	P	160
421	GGC	TCC	ACA	CCA	TCA	CCA	CCG	TCT	TCA	GGG	AAC	AGA	ACT	TCC	GGT	GAC	GGT	GGC	TCA	CCT	480
161	S	P	P	R	S	I	S	P	P	Q	N	S	G	D	S	D	S	S	S	G	180
481	TCA	CCA	CCT	CGG	TCG	ATA	AGC	CCT	CCT	CAG	AAT	AGT	GGA	GAT	TCA	GAC	TCA	TCA	TCG	GGG	540
181	L	L	L	L	L	A	V	C	I	C	I	C	C	N							200
541	CTT	TTG	CTT	CTA	CTT	GCA	GTG	TGT	ATT	TGC	ATC	TGT	TGC	AAC	AGG	AAG	AAG	AAG	AAG	AAA	600
201	S	P	Q	V	N	H	M	H	Y	Y	N	N	N	P	Y	G	G	A	P	S	220
601	TCT	CCT	CAG	GTC	AAC	CAC	ATG	CAC	TAC	TAC	AAT	AAC	AAT	CCT	TAT	GGA	GGA	GCA	CCC	TCA	240
221	G	N	G	G	Y	Y	K	G	T	P	Q	D	H	V	V	N	M	A	G	Q	260
661	GGT	AAT	GGT	GGT	TAT	TAC	AAG	GGA	ACA	CCT	CAA	GAT	CAT	GTG	GTG	AAT	ATG	GCT	GGT	CAA	720
241	G	G	G	N	W	G	P	Q	Q	P	V	S	G	P	H	S	D	A	S	N	280
721	GGA	GGT	GGG	AAT	TGG	GGT	CCA	CAG	CAA	CCT	GTG	TCT	GGT	CCT	CAC	AGT	GAT	GCT	TCC	AAC	300
261	L	T	G	R	T	A	I	P	S	P	Q	A	A	T	L	G	H	N	Q	S	320
781	TTA	ACC	GGT	CGA	ACT	GCT	ATA	CCG	TCA	CCT	CAA	GCT	GCA	ACT	CTT	GGT	CAC	AAC	CAA	AGC	340
281	T	F	T	Y	D	E	L	S	I	A	T	E	G	F	A	Q	S	N	L	L	360
841	ACT	TTT	ACA	TAC	GAT	GAA	CTG	TCC	ATT	GCA	ACA	GAA	GGT	TTT	GCT	CAG	TCA	AAT	TTG	CTA	380
301	G	Q	G	G	F	G	Y	V	H	K	G	V	L	P	S	G	K	E	V	A	400
901	GGA	CAA	GGA	GGA	TTT	GGG	TAT	GTT	CAT	AAA	GGA	GTT	CTG	CCT	AGT	GGC	AAA	GAA	GTT	GCA	420
321	V	K	S	L	K	L	G	S	G	Q	G	E	R	E	F	Q	A	E	V	D	440
961	GTG	AAG	AGT	CTT	AAA	CTT	GGA	AGT	GGA	CAA	GGG	GAA	CGC	GAG	TTT	CAA	GCA	GAG	GTT	GAT	460
341	I	I	S	R	V	H	H	R	H	L	V	S	L	V	G	Y	C	I	S	G	480
1021	ATC	ATT	AGC	CGT	GTC	CAT	CAT	CGT	CAT	CTC	GTT	TCT	CTT	GTT	GGA	TAT	TGC	ATC	TCT	GGT	500
361	G	Q	R	L	L	V	Y	E	F	I	P	N	N	T	L	E	F	H	L	H	520
1081	GGT	CAA	AGA	CTT	TTG	GTT	TAT	GAG	TTT	ATA	CCT	AAC	AAC	ACT	CTT	GAA	TTT	CAT	CTT	CAT	540
381	G	K	G	R	P	V	L	D	W	P	T	R	V	K	I	A	L	G	S	A	560
1141	GGA	AAG	GGT	CGT	CCG	GTT	TTG	GAT	TGG	CCT	ACA	AGA	GTG	AAG	ATT	GCA	TTG	GGA	TCA	GCT	580
401	R	G	L	A	Y	L	H	E	D	C	K	K	I	F	I	S	H	I	C	I	600
1201	AGA	GGC	CTT	GCA	TAT	TTG	CAT	GAA	GAG	TGT	AAG	AAA	ATC	TTT	ATC	TCA	CAT	ATT	TGC	ATC	620
421	S	H	P	R	I	I	H	R	D	I	K	A	A	N	I	L	L	D	F	S	640
1261	AGT	CAC	CCT	CGC	ATT	ATC	CAC	AGA	GAT	ATC	AAA	GCT	GCA	AAC	ATT	CTT	CTT	GAT	TTT	AGT	660
441	F	E	T	K	V	A	D	F	G	L	A	K	L	S	Q	D	N	Y	T	H	680
1321	TTT	GAG	ACC	AAG	GTG	GCA	GAT	TTT	GGA	TTG	GCT	AAG	CTA	TCT	CAA	GAC	AAC	TAT	ACT	CAT	700
461	V	S	T	R	V	M	G	T	F	G	Y	L	A	P	E	Y	A	S	S	G	720
1381	GTC	TCC	ACT	CGC	GTC	ATG	GGA	ACT	TTT	GGA	TAC	TTA	GCT	CCA	GAG	TAT	GCA	TCA	AGC	GGA	740
481	K	L	S	D	K	S	D	V	F	S	F	G	V	M	L	L	E	L	I	T	760
1441	AAG	TTA	TCC	GAC	AAA	TCT	GAT	GTT	TTC	TCA	TTT	GGA	GTA	ATG	CTT	CTT	GAG	CTC	ATA	ACC	780
501	G	R	P	P	L	D	L	T	G	E	M	E	D	S	L	V	D	W	A	R	800
1501	GGA	AGA	CCT	CCT	CTG	GAT	CTA	ACT	GGA	GAA	ATG	GAA	GAT	AGC	TTG	GTA	GAT	TGG	GCA	AGG	820
521	P	L	C	L	K	A	A	Q	D	G	D	Y	N	Q	L	A	D	P	R	L	840
1561	CCT	TTG	TGT	TTG	AAA	GCA	GCT	CAA	GAT	GGA	GAT	TAC	AAC	CAA	TTG	GCT	GAT	CCA	CGT	CTA	860
541	E	L	N	Y	S	H	Q	E	M	V	Q	M	A	S	C	A	A	A	A	I	880
1621	GAG	CTA	AAC	TAC	AGT	CAT	CAA	GAG	ATG	GTT	CAA	ATG	GCT	TCT	TGT	GCA	GCT	GCA	GCA	ATC	900
561	R	H	S	A	R	R	R	P	K	M	S	Q	V	Q	K	L	I	P	L	V	920
1681	AGA	CAT	TCA	GCA	AGA	AGA	CGG	CCT	AAG	ATG	AGC	CAG	GTT	CAA	AAA	CTC	ATA	CCA	CTT	GTT	940
581	G	S	I	I	V	R	A	L	E	G	D	M	S	M	D	D	L	S	E	G	960
1741	GGT	TCT	ATT	ATT	GTA	CGA	GCA	CTA	GAA	GGA	GAT	ATG	TCA	ATG	GAT	GAT	CTA	AGT	GAG	GGA	980
601	T	R	P	G	Q	S	T	Y	L	S	P	G	S	V	S	S	E	Y	D	A	1000
1801	ACA	AGA	CCA	GGA	CAA	AGC	ACG	TAC	TTG	AGC	CCC	GGG	AGC	GTG	AGC	TCA	GAG	TAT	GAC	GCA	1020
621	S	S	Y	T	A	D	M	K	K	F	K	K	L	A	L	E	N	K	E	Y	1040
1861	AGC	TCG	TAC	ACG	GCA	GAC	ATG	AAA	AAG	TTT	AAG	AAA	CTG	GCG	TTA	GAG	AAT	AAA	GAA	TAT	1060
641	Q	S	S	E	Y	G	G	T	S	E	Y	G	L	N	P	S	A	S	S	S	1080
1921	CAA	AGC	AGT	GAA	TAT	GGT	GGA	ACA	AGT	GAG	TAT	GGC	TTA	AAC	CCT	TCT	GCT	TCA	AGT	AGT	1100
661	E	E	M	N	R	G	S	M	K	R	N	P	Q	L							1120
1981	GAA	GAA	ATG	AAT	AGA	GGC	TCA	ATG	AAA	CGC	AAT	CCT	CAG	CTT	TGA						1140

Figure 13B

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Figure 14A
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1	M	S	L	S	P	S	S	S	P	A	P	A	T	S	P	P	A	M	S	L	20	
1	ATG	TCG	CTC	TCT	CCT	TCT	TCC	TGG	CCG	GCT	CCG	GCA	ACT	TCC	CCG	CCT	GCC	ATG	TCA	TTA	60	
21	P	P	A	D	S	V	P	D	T	S	S	P	P	A	P	P	L	S	P	L	40	
61	CCT	CCG	GCA	GAT	TCC	GTA	CCT	GAC	ACG	TCA	TCA	CCT	CCA	GCT	CCT	CCT	TTG	TCT	CCT	CTT	120	
41	P	P	P	L	S	S	P	P	P	L	P	S	P	P	P	L	S	A	P	T	60	
121	CCC	CCA	CCA	TTG	AGC	TCT	CCT	CCG	CCG	TTG	CCT	TCA	CCA	CCG	CCT	CTC	TCC	GCT	CCC	ACC	180	
61	A	S	P	P	P	L	P	V	E	S	P	P	S	P	P	I	E	S	P	P	80	
181	GCT	TCC	CCA	CCG	CCT	CTT	CCG	GTT	GAA	TCC	CCA	CCG	TCT	CCT	CCT	ATA	GAA	TCA	CCA	CCG	240	
81	P	P	L	L	E	S	P	P	P	P	P	L	E	S	P	S	P	P	S	P	100	
241	CCT	CCT	CTA	CTG	GAA	TCA	CCT	CCT	CCT	CCT	CCG	TTG	GAA	TCT	CCA	TCT	CCA	CCG	TCT	CCT	300	
101	H	V	S	A	P	S	G	S	P	P	L	P	F	L	P	A	K	P	S	P	120	
301	CAC	GTC	TCA	GCT	CCT	TCC	GGT	TCA	CCG	CCA	TTA	CCC	TTT	CTT	CCC	GCC	AAA	CCT	TCT	CCG	360	
121	P	P	S	S	P	P	S	E	T	V	P	P	G	N	T	I	S	P	P	P	140	
361	CCG	CCT	TCT	TCA	CCT	CCC	TCC	GAG	ACA	GTT	CCG	CCG	GGA	AAT	ACG	ATT	TCT	CCA	CCA	CCT	420	
141	R	S	L	P	S	E	S	T	P	P	V	N	T	A	S	P	P	P	P	S	160	
421	CGT	TCA	CTT	CCC	TCC	GAA	TCA	ACC	CCG	CCG	GTG	AAC	ACA	GCT	TCT	CCT	CCA	CCG	CCA	TCT	480	
161	P	P	R	R	R	S	G	P	K	P	S	P	P	P	P	I	N	S	S	P	180	
481	CCT	CCT	CGC	CGC	CGT	AGT	GGC	CCT	AAG	CCT	TGG	TTT	CCT	CCT	CCC	ATC	AAT	TCT	TCT	CCA	540	
181	P	N	P	S	P	N	T	P	S	L	P	E	T	S	P	P	P	P	K	P	200	
541	CCA	AAT	CCT	TCT	CCG	AAC	ACT	CCG	TCA	CTC	CCA	GAA	ACT	TCT	CCT	CCA	CCT	AAA	CCA	CCG	600	
201	L	S	T	T	P	F	P	S	S	S	T	P	P	P	K	K	S	P	A	A	220	
601	CTC	TCA	ACG	ACG	CCA	TTT	CCC	TCC	TCA	TCC	ACT	CCC	CCG	CCT	AAG	AAG	TCC	CCT	GCA	GCA	660	
221	V	T	L	P	F	F	G	P	A	G	Q	L	P	D	G	T	V	A	P	P	240	
661	GTA	ACT	CTT	CCT	TTT	GGG	CCA	GCG	GGC	CAA	TTA	CCG	GAT	GGG	ACC	GTA	GCA	CCT	CCT	720		
241	I	G	P	V	I	E	P	K	T	S	P	A	E	S	I	S	P	G	T	P	260	
721	ATT	GGG	CCT	GTT	ATA	GAG	CCC	AAG	ACG	AGT	CCA	GCC	GAA	TCA	ATA	TCT	CCG	GGA	ACG	CCA	780	
261	Q	P	L	V	P	K	S	L	P	V	T	T	S	Y	H	R	S	S	A	G	280	
781	CAG	CCA	CTG	GTT	CCG	AAG	AGT	CTA	CCT	GTA	ACG	ACG	TGG	TAT	CAC	TCA	TCC	GCC	GGA	840		
281	F	L	F	G	G	V	I	V	G	A	L	L	L	I	L	L	G	L	L	P	300	
841	TTT	TTA	TTT	GGC	GGT	GTA	ATC	GTT	GGA	GCT	CTT	CTA	CTA	ATT	CTG	TTA	GGT	CTT	CTC	TTT	900	
301	V	F	Y	R	A	T	R	N	R	N	N	N	S	S	S	A	H	H	Q	S	320	
901	GTC	TTC	TAC	AGA	GCT	ACC	AGA	AAT	AGA	AAT	AAC	AAC	AGC	AGC	TCT	GCT	CAT	CAT	CAA	TCC	960	
321	K	T	P	S	K	V	Q	H	H	R	G	G	N	A	G	T	N	Q	A	H	340	
961	AAA	ACT	CCC	TCA	AAA	GTT	CAA	CAT	CAT	CCG	GGC	GGT	AAT	GCT	GGT	ACG	AAC	CAG	GCA	CAT	1020	
341	V	I	T	M	P	P	P	I	H	A	K	Y	I	S	S	G	G	C	D	T	360	
1021	GTT	ATC	ACA	ATG	CCA	CCA	ATC	CAT	GCT	AAA	TAT	ATA	TCT	AGT	GGA	GGT	TGT	GAT	ACG	1080		
361	K	E	N	N	S	V	A	K	N	I	S	M	P	S	G	M	F	S	Y	E	380	
1081	AAG	GAG	AAC	AAT	TCT	GTT	GCG	AAA	AAC	ATT	TCA	ATG	CCA	TCT	GGA	ATG	TTC	TCC	TAC	GAA	1140	
381	E	L	S	K	A	T	G	G	F	S	E	E	N	L	L	G	E	G	G	F	400	
1141	GAA	CTT	TCA	AAA	GCA	ACT	GGT	GGA	TTT	TCA	GAG	GAG	AAC	CTT	TTG	GGA	GAA	GGC	GGT	TTT	1200	
401	G	Y	V	H	K	G	V	L	K	N	G	T	E	V	A	V	K	Q	L	K	420	
1201	GGA	TAT	GTT	CAC	AAA	GGA	GTG	TTG	AAA	AAC	GGG	ACA	GAA	GTT	GCG	GTG	AAG	CAG	CTG	AAG	1260	
421	I	G	S	Y	Q	G	E	R	E	F	Q	A	E	V	D	T	I	S	R	V	440	
1261	ATT	GGG	AGC	TAT	CAA	GGG	GAA	AGA	GAA	TTT	CAA	GCT	GAG	GTT	GAC	ACA	ATC	AGT	AGG	GTT	1320	
441	H	H	K	H	L	V	S	L	V	G	Y	C	V	N	G	D	K	R	L	L	460	
1321	CAT	CAT	AAG	CAC	CTC	GTT	TCA	TTG	GTT	GGT	TAT	TGC	GTT	AAT	GGA	GAT	AAA	AGA	CTC	TTG	1380	
461	V	Y	E	F	V	P	K	D	T	L	E	F	H	L	H	E	N	R	G	S	480	
1381	GTT	TAC	GAG	TTT	GTT	CCT	AAA	GAT	ACC	TTG	GAG	TTT	CAC	TTG	CAT	GAG	AAC	AGA	GGA	AGC	1440	
481	V	L	E	W	E	M	R	L	R	I	A	V	G	A	A	K	G	L	A	Y	500	
1441	GTG	TTG	GAA	TGG	GAA	ATG	AGG	CTC	AGG	ATT	GCT	GTA	GGA	GCA	GCA	AAA	GGA	TTA	GCT	TAT	1500	
501	L	H	E	D	C	S	P	T	I	I	H	R	D	I	K	A	A	N	I	L	520	
1501	CTT	CAT	GAG	GAT	TGC	AGT	CCA	ACT	ATA	ATT	CAC	CGT	GAT	ATC	AAA	GCA	GCT	AAT	ATC	CTT	1560	
521	L	D	S	K	F	E	A	K	V	S	D	F	G	L	A	K	F	F	S	D	540	
1561	CTA	GAT	TCC	AAA	TTT	GAG	GCA	AAG	GTC	TCT	GAC	TTT	GGA	CTA	GCC	AAG	TTT	TTC	TCA	GAC	1620	
541	T	N	S	S	P	T	H	I	S	T	R	V	V	G	T	F	G	Y	M	A	560	
1621	ACC	AAT	TCA	TCA	TTC	ACT	CAT	ATC	TCT	ACT	CGA	GTG	GTA	GGA	ACT	TTC	GGA	TAC	ATG	GCT	1680	
561	P	E	Y	A	S	S	G	K	V	T	D	K	S	D	V	Y	S	F	G	V	580	
1681	CCA	GAA	TAC	GCG	TCC	AGT	GGT	AAA	GTA	ACT	GAT	AAA	TCA	GAT	GTA	TAT	TCC	TTT	GGG	GTC	1740	
581	V	L	L	E	L	I	T	G	R	P	S	I	P	A	K	D	S	S	T	N	600	
1741	GTG	CTT	CTA	GAA	CTC	ATC	ACT	GGA	CGT	CCA	TCA	ATT	TTC	GCC	AAA	GAT	TCT	TCC	ACA	AAC	1800	
601	Q	S	L	V	D	W	A	R	P	L	L	T	K	A	I	S	G	E	S	F	620	
1801	CAG	AGT	TTA	GTA	GAC	TGG	GCG	AGG	CCA	TTG	CTT	ACG	AAA	GCA	ATC	TCT	GGA	GAA	AGT	TTT	1860	
621	D	F	L	V	D	S	R	L	E	K	N	Y	D	T	T	Q	M	A	N	M	640	
1861	GAC	TTT	CTT	GTA	GAC	TCA	AGG	TTG	GAG	AAG	AAT	TAC	GAT	ACA	ACT	CAG	ATG	GCA	AAC	ATG	1920	
641	A	A	C	A	A	A	C	I	R	Q	S	A	W	L	R	P	R	M	S	Q	660	
1921	GCT	GCT	TGT	GCT	GCT	GCT	TGC	ATA	CGC	CAA	TCA	GCT	TGG	CTT	CGG	CCT	AGA	ATG	AGC	CAG	1980	
661	V	V	R	A	A	L	E	G	E	V	A	L	R	K	V	E	E	T	G	N	S	680
1981	GTA	GTA	CGT	GCT	CTT	GAA	GGC	GAG	GTG	GCC	CTG	AGA	AAG	GTC	GAA	GAG	ACT	GGG	AAT	AGC	2040	
681	V	T	Y	S	S	S	E	N	P	N	D	I	T	P	R	Y	G	T	N	K	700	
2041	GTG	ACC	TAT	AGC	TCT	TCT	GAA	AAC	CCG	AAT	GAC	ATC	ACA	CCA	CGG	TAT	GGA	ACA	AAT	AAG	2100	
701	R	R	F	D	T	G	S	S	D	G	Y	T	S	E	Y	G	V	N	P	S	720	
2101	AGG	AGA	TTC	GAC	ACA	GGT	TCA	AGC	GAT	GGT	TAC	ACT	TCA	GAA	TAT	GGA	GTT	AAC	CCT	TCT	2160	
721	Q	S	S	S	E	H	Q	Q	V	N	T	*									732	
2161	CAG	TCG	AGC	AGT	GAA	CAT	CAA	CAG	GTG	AAT	ACT	TAG									2196	

Figure 14B

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